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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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2674
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1: /cgn2_6/ptodata/2/pubpna/US07_N

2: /cgn2_6/ptodata/2/pubpna/US06_

3: /cgn2_6/ptodata/2/pubpna/US06_
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Copyright (c) 1993 - 2005 Compugen Ltd.
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 18 derived by analysis of the total score distribution.

## SUMMARIES

110 100 110 110	Result No.
232674 232674 362.4 362.4 362.5 296.2 296.2 296.2 271.6 201.2	Score
100.0 100.0 87.0 13.6 13.6 12.2 11.1 11.1 11.1 11.1 17.5 7.5	Query
2674 2674 2889 15297 15297 15297 15297 15297 1449 361 1779 381 1779 2955	Query Match Length DB
13 17 16 17 17 17 17 18	BB
US-10-003-295-1 US-10-660-763-1 US-10-240-965-256 US-10-003-295-3 US-10-660-763-3 US-09-918-995-1503 US-09-948-802-5 US-10-121-925-5 US-10-121-925-5 US-10-131-510-525 US-10-1384-339C-1	ID
Sequence 1, Appli Sequence 1, Appli Sequence 256, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1503, Ap Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 555, Appli Sequence 575, Appli Sequence 1, Appli	Description

198 7.4 3370 16 US-10-354-358-101 198 7.4 3370 16 US-10-210-120-19 198 7.4 3370 18 US-10-776-827-82 198 7.4 3370 18 US-10-776-827-82 198 7.4 3370 18 US-10-776-827-82 198 7.4 6.9 3042 18 US-10-364-39C-2 185.4 6.9 3921 10 US-10-269-909-19 185.4 6.9 3921 17 US-10-362-887-1036 185.4 6.9 3921 17 US-10-362-887-1036 185.4 6.9 3921 17 US-10-372-218-1036 185.4 6.9 3921 18 US-10-648-591 185.4 6.9 3921 18 US-10-473-974-223 185.4 6.9 3921 18 US-10-473-974-223 185.4 6.9 3921 18 US-10-473-974-223 185.4 6.9 3921 18 US-10-648-591 185.4 6.9 3921 18 US-10-488-7-1036 185.4 6.9 3921 18 US-10-473-974-223 185.4 6.9 3921 18 US-10-280-26-31 185.4 6.9 3921 18 US-10-280-576-24 185.4 6.9 3921 19 US-10-6848-591 174.6 6.5 1050 18 US-10-377-268-3 174.6 6.5 3416 18 US-10-377-268-3 174.6 6.5 3416 17 US-10-325-430-8 174.6 6.5 3416 17 US-10-325-430-8 174.6 6.5 3416 17 US-10-305-720-1483 174.6 6.5 3416 17 US-10-291-803-51 174.6 6.5 3416 17 US-10-291-803-51 174.6 6.5 4151 18 US-10-476-962-3 174.6 6.5 4151 18 US-10-476-962-3 174.6 6.4 1611 18 US-10-497-641-1	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
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PULU 3 3 5 7 1 5 1 2 2 2 2 3 2 1 3 2 1 3 2 1 3 2 2 3 2 3	, Appli	•	•	•	•	2, Appi	, Appl:	3, App.	1, App	483, Ap	, Appli	, Appl:	Appli	, Appl:	, Appli	Appl:	-	, Appli	, Appl		<ol> <li>Appl:</li> </ol>	119, Apj	1036, Ap	036, AJ	, Appl	9, App	22, Apı	9, App	Appli	19, App	•	•	۲

## ALIGNMENTS

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; ORGANISM: Homo sapiens
US-10-003-295-1
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US-10-003-295-1
                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/10003295
Publication No. US20020168741A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01183DIV
CURRENT APPLICATION NUMBER: US/10/003,295
CURRENT APPLICATION NUMBER: US/10/003,295
CURRENT FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2674
                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 2674; Conservative
121 AGCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGC
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                                                             GGAACAGCACTATGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGC 120
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0; Mismatches
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1201 TGCAGGCCCAGCÀGGAGTTGCTGGAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCCC 1260	1141 GGCAAGTGCTGCAAGAAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGGCCAGGCCAAGC 1200	1081 AGCTCCGGAATGAAGAGGAGAACACCCACCCCGGGAGCGGGTGCAGCTGCTGGGCAAGA 1140	1021 TGGCTGTGGCCACCGAGATGGTTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGG 1080	961 AGCTGAACGAGCTGACTGTGGAGAGCGTGCAGCACCACGCTGACCTCAGTGACAGATGAGC 1020	901 GTGTCACGTTCGATGAGTCACTTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGAGCTCC 960	841 CTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGACCCTGACGTCCCACCCT. 900	781 TGCAGGATGAGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCCCGCATCCAGC 840	721 AGGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGG 780	661 ACCAGCACCACCAGCTCCTGCTGCCGGCCTGCTGCGGTCACTGCAGGACCTGCAGG 720	601 GGAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGGCGTGCGGGGCTGCGCAGCTACACC 660	541 AGGAGGCCAGCAAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGT 600	481 AGCTGAAGAGCCAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAGCGCAAGTACC 540	421 GCGAGCAGTGGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGA 480	361 GGCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACA 420 	301 CCAGCCAAACTGAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAG 360	241 GGGGCCAGAGCCGGGCCATCAGCCCTGACAGCCCCATCAGTCAG	121 AGCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGAATGGCCCAGC 180  181 GGGTCAAGAGTGACAGGGAGTATGCAGGACTGCCTTCACCACATGTCCCTGCAGGACAGTG 240
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Query Match Best Local Similarity 100.0%; Prod. No. 0; Best Local Similarity 100.0%; Prod. No. 0; Matches 2674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 TCCGGGGTCCGCACCGGGCCTGAGTCGGTCCCAGGAGCAGCTGCCCGTGC 60 1	US-10-660-763-1  Sequence 1, Application US/10660763  Publication No. US20040063130A1  GENERAL INFORMATION: APPLICANT: GAN, Weiniu et al.  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  TITLE OF INVENTION: THEREOF  FILE REFERENCE: CL001183DIVII  CURRENT APPLICATION NUMBER: US/30/660,763  CURRENT FILING DATE: 2003-09-12  NUMBER OF SEQ ID NOS: 4  SOFTWARE: FASTSEQ for Windows Version 4.0  SEQ ID NO 1  LENGTH: 2674  TYPE: DNA  ORGANISM: Homo Sapiens  US-10-660-763-1	Qy         2341         CCCTTCTCAAGCTGGTGGCCTCTGCAAGGCCTAGGTGCAGCTCCAGCTCA         2400           Db         2341         CCCTTCTCAAGCTGGTGGCCTCTGCAGGCCTAGGTGCAGCTCCTAGCGGCTCCAGCTCA         2400           Qy         2401         TATGCTGACAGCTCTTCACAGTCCTGGACTCCTGCCACCAGCTCCACACTGCCGGCAGG         2460           Db         2401         TATGCTGACAGCTCTTCACAGTCCTGGACTCCTGCCACCAGCATCCACACTGCCGGCAGG         2460           Qy         2461         ATGCAGCGCTGTTCCTCTTCTGTGTTCCTGCTGCCACCAGCATCCACACTGCCGGCAGG         2460           Qy         2461         ATGCAGCGCCGTGTCCTCTTCTGTGTTCCCTGCTGCCACGGCTTCCTCTTCCGGGCAGA         2520           Qy         2461         ATGCAGCGCCGTGTCCTCTTGTGTCCCTGCTGCTGCCAGGGCTTCCTCTTCCGGGCAGA         2520           Qy         2521         AACAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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ATGCAGCGCCGTGTCCTCTCTGTGTCCCTGCTGCTGCCAGGGCTTCCTCCTTCCGGGCAGA
                                                ATGCAGCGCCGTGTCCTCTGTGTGCCCTGCTGCTGCCAGGGCTTCCTCTTCCGGGCAGA
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Sequence 256, Application US/10240965

Publication No. US20030165924A1

GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: SHIFFMAN, Dov
APPLICANT: SHIFFMAN, Dov
APPLICANT: SEILHAMER, Jeffrey J.
APPLICANT: SEILHAMER, Jeffrey J.
APPLICANT: PORTER, Gordon J.
APPLICANT: MIKITA, Thomas J.
APPLICANT: TAI, Julie
TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
FILE REFERENCE: PA-0025 PCT
CURRENT APPLICATION NUMBER: US/10/240,965
CURRENT PILING DATE: 2002-10-04
PRIOR APPLICATION UNUMBER: 60/195,106
PRIOR APPLICATION UNUMBER: 60/195,106
PRIOR APPLICATION NUMBER: 60/195,106
PRIOR APPLICATION NUMBER: 50/195,106
PRIOR APPLICATION ONUMBER: 50/195,106
PRIOR PEILING DATE: 2000-04-05
SOFTWARE: PERL PROGram
SEQ ID NO 256
LENGTH: 2889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANIEM; Homo sapiens
; FEATURE;
; NAME/KEY; misc feature
; OTHER INFORMATION: Incyte ID No. US20030165924A1 997347.6
US-10-240-965-256.
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US-10-240-965-256
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Best Local Similarity
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                                                                      CAGCCAAACTGA-GGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAG
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92.3%;
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2371 TAGGTGCAGCTCCTCAGCGGCTCCATATGCTGACAGCTCTTCACAGTCCTGGACT 2430	1558 AGCAGCTGTGGTACCACGGGGCCATCCCGAGGGCAGAGGTGGCTGAGCTGCTGGTGCACT 1617  1392 1391	g g
2638 TCCGAAAGCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCAGGCC	92	3 8
2311 TCCGAAAGCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCAGG	98 CCAAGTTCTCGCTCCCTCCACCGCTGCAGCTCATTCCGGAGGTGCAGAAGCCCCTGCATG 1557	, B
2578 GGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAGAGCA	1381 CCAAGTTCTCG 1391   Db	Ş
2518 GCGTCTGCCCCAGAGCTGTGTCTGATGCCGTGTTCAGGCTGATGGAGCAGTGTA	1321 AGGGGGAAGGACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCC 1380	8
2130 GGGCTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAGTG	78 CGCCTGTGCTGCTGCAGGATGACCGCCACTCCACGTCGTCCTCGGAGCAGGAGCAGGAGCAGA	
2131 GGGCCTCCCCCTATCCCAACCTCAGCAATAGCAGCAGAACACGGGAGTTTGTGGAGAAGGGGG	61 CGCCTGTGCTGCTGCAGGATGACCGCCACTCCACGTCGTCCTCGGAGCGAGC	<b>9</b> ;
2398 ACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTCTGGAGACCTTCAGCCTGG	1201 TGCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCCC 1260	B 8
2338 GGGGCCTCAGACAGTCCCCGTGAAGTGGACCGCACCTGAGGCCCCTTAACTACCGCCGCT	1141 GGCAAGTGCTGCAAGAAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGGCCAGGCCAAGC 1200	음 성
	1081 AGCTCCGGAATGAAGAGGAGAACACCCACCCCGGGAGCCGGTGCAGCTGCTGGGCAAGA 1140	용 성
	1021 TGGCTGTGGCCACCGACATGGTTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGG 1080	<u> </u>
	1 AGCTGAACGAGCTGACTGTGGAGAGCGTGCACCACACGCTGACCTCACTGACAGGATGAGC 1020	8 8
98 31	01 GTGTCACGTTCGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGAGCTCC 960	B 8
2038 CCAACATCGTGCGTCTCATTGGTGTCTGCACCCTACACGGACGG	841 CTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCT 900	용 성
1711 CCAACATCGTGCGTCTCATTGGTGTCTGCACGACCAGAAGCAGCCCATCTACATCGTCATGG	781 TGCAGGATGAGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCCCGCATCCAGC 840	8 8
	721 AGGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGG 780	B 8
1858 ACCATGAGGACCTGGTGATGAGTGAGTGATGAACTTTTTTTT	661 ACCAGCACCACCACCACCTGCTGCCCGGCCTGCTGCGGTCACTGCAGGACCTGCACG 720	₿ <i>8</i>
1798 TCACCAAGAAGTGTGTGTGTGCCCAAGACTGGGGGAAAGTGTTCA  1798 TCACCAAGAAGAGTGTGTTGTCCTGCACAGGGCTGTGCCCAAGAACTTGGGGAAAGTGTTCA  1531 ACCATGAGGACCTGGTGTTGGGTAAGCAAATTGGACGGGGAAACTTTGGCGAAGTGTTCA	601 GGAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCGCCAGCTACACC 660	B 8
	541 AGGAGGCCAGCAAAGACAAGGACCGTGACCAAGGCCAAGGACAAGTATGTGCGCAGCCTGT 600	B 8
1678 GGGATGGTCTGCCCCGGCACTTCATCATCCAGTCCTTGGATAACCTGTACCAGCCAG	481 AGCTGAAGAGCCAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCCAAGCGCAAGTACC 540	용 성
1618 CTGGGGACTTCCTGGTGCGGGAGAGCCAGGGCAAGCAGGAGTACGTGCTGTCGGTGCTGT	421 GCGAGCAGTIGGAGCAGCAGCAGCACGACAGCACGAGCACAGCAC	₽ 5
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RESULT 5
US-10-660-763-3
; Sequence 3, Application US/10660763
; Publication No. US20040063130A1
; GENERAL INFORMATION:
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; TYPB: DNA
; ORGANISM: Homo sapiens
US-10-003-295-3
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US-10-003-295-3
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Publication US/20020168741A1
GENERAL INFORMATION:
APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01183DIV,
CURRENT APPLICATION NUMBER: US/10/003,295
CURRENT FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 4
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Best Local Similarity
Matches 363; Conserv
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Pred. No. 1.2e-46;
0; Mismatches 1;
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APPLICANT: Hyseq, Inc.

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 1503

LENGTH: 449

TYPE: DNA

ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   US-09-918-995-1503
Sequence 1503, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CLOO1183DIVII CURRENT APPLICATION UNMEER: US/10/660,763

CURRENT APPLICATION WHEER: US/10/660,763

CURRENT FILING DATE: 2003-09-12

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FBSESEQ for Windows Version 4.0

SEQ ID NO 3
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(449)
OTHER INFORMATION: n = A,T,C
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Pred. No. 1.2e-46;
0; Mismatches 1
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US-09-948-802-5
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Publication No. US20020172981A1

GENERAL INFORMATION:

APPLICANT: ROBISON, KEITH E.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR FILE REFERENCE: MNI-090

CURRENT APPLICATION NUMBER: US/09/948,802

CURRENT FILING DATE: 1999-08-31

RUMBER OF SEQ ID NOS: 18

NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 361
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: All occurences of n indicate any nucleotide
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ACTGCCTGGTGACAGAAGAATGTCCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA 1981
                                                         CTGCTGGCATGGAGTACCTGGAGAGAGAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA 1923
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                                 CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA
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Sequence 5. Application US/10121925

PHUBLICATION NO. US20030104505A1

GENERAL INFORMATION:
APPLICANT: ROBISON, KEITH E.

ITILE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR FILE REFERENCE: MNI-090

CURRENT FILING DATE: 2002-04-12

PRIOR APPLICATION NUMBER: US/99/948,802

PRIOR APPLICATION NUMBER: US/99/948,802

PRIOR APPLICATION NUMBER: 09/87,212

PRIOR APPLICATION NUMBER: 09/87,212

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

SEQ ID NO 5

LENGTH: 361

TYPE: DNA

ORGANISM: Homo sapiens

PEATURE:

OTHER INFORMATION: All occurences of n indicate any nucleotide

OTHER INFORMATION: All occurences of n indicate any nucleotide
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US-10-280-576-19

; Sequence 19, Application US/10280576
; Publication No. US20040044405A1
; GENERAL INFORMATION:
; APPLICANT: Wolff, Matthew R.
; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COFFILE REFERENCE: 09820.189
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/343,732

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NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.:
SEQ ID NO 19
LENGTH: 1779
1678
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RESULT 10
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; Sequence 525, Application US/10101510
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APPLICANT: WAN, JACKSON
APPLICANT: WANG, YIXIN
APPLICANT: WANG, YIXIN
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
CURRENT PELLORATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
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SEQ ID NO 525
LENGTH: 3875
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Best Local Similarity 54.9%;
Matches 423; Conservative
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Pred. No. 6.6e-22;
0; Mismatches 338;
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US-10-384-339C-1
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PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: DE 10155280.7
PRIOR FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: DE 10158411.3
PRIOR APPLICATION NUMBER: DE 10160151.4
PRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 173
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SEQ ID NO 1
LENGTH: 2955
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Best Local Similarity 54.7%;
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
TITLE: Eph A1
PATENT DOCUMENT NUMBER: NM00532
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TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: 20200/2002
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PRIOR FILING DATE: 2002-01-09
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TGAACTACCTCAGTAATCACAATTATGTCCACCGGGACCTGGCTGCCAGAAACATCTTGG
                              TGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGAACTGCCTGG 1932
                                                                 GGGAGGACCAGCTGGTCCCTGGGCAGCTAGTGGCCATGCTGCAGGGCATAGCATCTGGCA
                                                                                       AGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAGCTGCTGGCA 1872
                                                                                                                                                                                                TGGGCCAGTTTAGCCACCCGCATATTCTGCATCTGGAAGGCGTCGTCACAAAGCGAAAGC
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Pred. No. 2e-21;
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; ORGANISM: Homo sapiens
US-09-967-768A-144
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RESULT 12
US-09-967-768A-144
; Sequence 144, Application US/09967768A
; Patent No. US20020150877A1
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CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 325
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Best Local Similarity 54.7%;
Matches 421; Conservative
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TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Sets
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                                               TGAAGCAGTACAGCCACACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGC 1752
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ĊĠATĊATGATĊACAĠAATTTATGGAĞAATĠCAĞCCCTGGATGCCTTCCTGAĞGGAĞC 2266
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FILE REFERENCE: MPIO2-020PIRNOWNIM
CURRENT APPLICATION NUMBER: US/10/354,358
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 60/353,600
PRIOR PILLING DATE: 2002-01-31
PRIOR PILLING DATE: 2002-01-31
PRIOR PILLING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/364,517
PRIOR PILLING DATE: 2002-04-09
PRIOR PILLING DATE: 2002-04-09
PRIOR PILLING DATE: 2002-04-10
PRIOR PILLING DATE: 2002-04-10
PRIOR PILLING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR APPLICATION NUMBER: US 60/374,194
PRIOR APPLICATION NUMBER: US 60/374,194
PRIOR PILLING DATE: 2002-04-16
PRIOR PILLING DATE: 2002-04-19
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APPLICANT: Williamson, Mark
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Rudolph-Owen, Laura A.
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: CANCER USING 140, 1470, 1886, 2089, 2427, 3702, 5891, 6428,
TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33220, 1586, 9943,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
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APPLICANT: MacBeth, Kyle J.
APPLICANT: TBai, Fong-Ying
APPLICANT: Lescon, Andrea
APPLICANT: Lightcap, Eric S.
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; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; Remaining Prior Application data removed - Se; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 3370
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Best Local Similarity
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ORGANISM: Homo
FEATURE:
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LOCATION: (94)...(3048)
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                            <u>AGTTTGTGGAGAAGGGGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCA</u>
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Sequence 19, Application US/10210120

Publication No. US20030175736A1

GENERAL INFORMATION:
APPLICANT: Chinnaiyan, Arul M.
APPLICANT: Rubin, Mark A.
APPLICANT: Rubin, Mark A.
APPLICANT: Rubin, Mark A.
APPLICANT: Secentumar, Arun
TITLE OF INVENTION: Expression Profile of Prostate Cancer
FILE REFERENCE: UM-07221
CURRENT APPLICATION NUMBER: US/10/210,120
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 60/309,581
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US 60/334,468
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NUMBER: US 60/334,468
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 123
SOOTWARE: Patentin version 3.2
LENGTH: 3370
TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 2e-21;
0; Mismatches 3
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US-10-776-827-82
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PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/214,870
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn version 3.1
SEQ ID NO 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 82, Application US/10776827
Publication No. US20040132086A1
GENERAL INFORMATION:
APPLICANT: Horwitz, Kathryn
APPLICANT: Richer, Jennifer
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Best Local Similarity
Matches 421; Conserv
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CURRENT FILING DATE: 2004-02-10
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ORGANISM: Homo sapiens
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TTGATGGCACATACGAAACCCAGGGAGGAAAGATCCCTATCCGTTGGACAGCCCCTGAAG 2506
                                      GGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAGG 2052
                                                                                                           TGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTTGGGATGTCCCGAGAGGAAGCCGATG
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Search completed: March 19, 2005, 19:55:48 Job time : 1398.78 secs	2233 GGCTCATGAAGCAGTGCTGGGCTATGAGCCTGGGCAGCCCAACTTC 2282	2173 AGTTTGTGGAGAAGGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCA 2232	2113 GGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACACGGG 2172	2053 CCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTCT 2112

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Result
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Listing first 45 summaries
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Match
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/FCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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CCAGCCAAA           CCAGCCAAA  GGCCCCTGA	GGCCAGA         GGCCAGA	GTCAAGA        GTCAAGA	CAAATGC         CAAATGC	AACAGCA        AACAGCA	CGGGGTC	Similarity 1; Conser	pplicati. 10584 MATION: MATION: NATION: NATION: NATION: CONTION: C		55555555555555555555555555555555555555
CCAAACTGAGGGCCTG	ecceseco	GTGACAGO         GTGACAGO	AGGAGGCC          AGGAGGCC	CTATGGG	cgcaccgo	100.0 y 100.0 rvative	on US/05 in et al ISCLATER ACID MC THEREOR THEREOR NUMBER: 2001 1 4 r Windov		25744 4 2 25744 4 3 25744 4 3 25744 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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	AGTCCTGGGCTGAGATCA 300 	ATGTCCCTGCAGGACAGTG 240 	AGAAAGTGGATGGCCCAGC 180	CAGGGCCACGGGGTCCTGC 120	CAGGAGCAGCTGCCCGTGC 60	Length 2674; Indels 0; Gaps 0	KINASE PROTEINS, AND USES		Sequence 2, Appli Sequence 2, Appli Sequence 8, Appli Sequence 8, Appli Sequence 9, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli

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CTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGGTGTTGTCCTGCACA 	ICGAACCTGTACCGACTGGAA 	A	CTCCTGCAGGATGAC             CTCCTGCAGGATGAC	CAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGG 	CAAGAAGCACTGCAGGG               CAAGAAGCACTGCAGGGG	CGGAATGAAGAGGAGAACACCCACCCCCGGGAGCGGTGCAGCTGCTGGG	TGGCTGTGGCCACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTG	AGCTGACTGTGGAGAGGCGTGCAGCACACGCTGACCTCAGTGACAGATGAG 	GATGAGTCACTGCTTGAGGAGGGTGAAC 	PACCAAGGCTTCCTGCGA                 TACCAAGGCTTCCTGCGA	TGCAGGATGAGGTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCGCATCCAG 	CTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGG	.ccagcaccaccaccagctcctgctgcccggcctgctgcggtcactgcagacctgcacq 	rcttigctcaccacaaccgctaigtgctgggcgigcgggctg 	gccagcaaagacaaggaccgtgac 	AGCCAGTACCGAGCTCTGGCA              AGCCAGTACCGAGCTCTGGCA	GGCCCCTGAGCAAGCTGAGCCTGATCCGGAAACGGCAGCAGCTTCGCAAGACCTACA GCGAGCAGTGGCAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGA 
CTCACCAAGAAGAGTGG           CTCACCAAGAAGAGTGG	CCGACTGGAAGGGGAAGGCTTTCCTAGG	CACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCI	OGCCACTCCACGTCGTCCTCGGAG	AAGCTGGAGCACCTGGG             AAGCTGGAGCACCTGGG	.gaagcactgcagggctgcaggtagcgctgtgcag 	CCCCGGGAGCGGGTGCA	CGGCAGGAGATGGTTACO	CAGCACACGCTGACCTC	GAGGGTGAACCGCTGGA              aagggtgaaccgctgga	CAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCC	GAGATGGCTGCAGCTGC             gagatggctgcagctgct	CTGCAGGAATACCTGGA 	GGCCTGCTGCGGTCACT( 	erecregecerecegec	GACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTG	GAGCTCTGGCACGGGACAGTGCCCAAGCCAAGCGCAAGTAC 	CGGGAACGGCAGCAGCTCCTCACCAAGACCCACAGGCTCACCAAGACCCACAG
TGTTGTCCTGCACA 150	CATTCCTTTGCTCA 1440             CATTCCTTTGCTCA 1440	AGGAATCTTCCGCC 138	GAGCAGGAGCGAG 132	GCCCGGCGAGCCCC 126	CAAGC 120       CAAGC 120	GCTGCTGGGCAAGA 1140             GCTGCTGGGCAAGA 1140	CAACAGG 108         AACAGG 108	AGTGACAGATGAGC 1020            AGTGACAGATGAGC 1020	CGCTGGAGCCTGGGGAGCTCC 960	IGACGTCCCACCCT 900                IGACGTCCCACCCT 900	TGCCCGCATCCAGC 840	ATTAGCAGCCTGG 780             	GCAGGACCTGCACG 720	TGCGCAGCTACACC 660	rerececaeccrer 600 	PAAGCGCAAGTACC 540	RCGCAAGACCTACA 420 CCAGGACATTGAGA 480                CCAGGACATTGAGA 480
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	CIGCIGCCAGGGCT	CTGCCACCAGCATC	TAGGTGCAGCTCCTC	TCCGAAAGCGGCATC	TOGGETATGAGCCTG	#GCCGTCTGCCCTGCC	GGCCTCCCCTATC		GGGGCTTCAGACAAG	TGAAGATCAGTGACT	AGTGCTGCATCACCG	TGAAGACTCTGCTGC	AGCTTGTGCAGGGGG	AGCTTGTGCAGGGGG	CAACATCGTGCTCAAGG		ACCATGAGGACCTGG

Qy 421 GCGAGCAGTGGCAGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGA 480	Oy  301 CCAGCCAAACTGAGGGCCTGAGCCGCTTGCTGCTGCGCAGAGGATCTGAACTCAG 360	Db 181 GGGCCAGAGCCGGGCCATCAGCCCTGACAGCCCCATCAGTCCTTGGGCTGAGAATCA 300  181 GGGGCCAGAGCCGGGCCATCAGCCCCTGACAGTCAGTCAG	61 GGAACAGCACTATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGC  121 AGCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGC	1 TCCGGGGTCCGCACCGGGCCTGAGTCGGTCCGAGGCCGTCCCAGGAGCAGCTGCCCGTGC 60	nila Co	CURRENT FILING DATE: 2001-12-06  NUMBER OF SEQ ID NOS: 4  SOFTMARE: FASTSEQ for Windows Version 4.0  SEQ ID NO 1  LENGTH: 2674  TYPE: DNA  ORGANISM: Homo sapiens	TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CL001183DIV CURRENT APPLICATION NUMBER: US/10/003,295	; sequence 1, Application US/10003295 ; Patent No. 6686187 ; GENERAL INFORMATION: ; APPLICANT: GAN, Weiniu et al. ; TITLE OF INVENTION INCLUDED UNIVAN VINNES DECORDING NUCLEUR	ESULT 2 S-10-003-295-1	Oy       2641 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	QY         2581         АЛАЛДЛАЛАЛДАЛАЛАЛДАЛАЛАЛДАЛАЛДАЛДАЛДАЛДА
Oy  1501 GGCTGTGCCCAAGGACAACTGCTTGAACAACCATGAGGACCTGGTTTGGTTCAGAACAACACCTGGTTTTGGTTCAGAACAACAACACCTGGTTTTGGTTCAGACAAGACAACTGATGATGAAGAACAACCTGGTTTTGGTTCAGCAGAACAACACCTGGTTTTGGTTCAGAGAACAACCTGGTTTTGGACAACAACCTGGTTTTGGAAGAACTTTTTGGCGAAAGTGTTCAGCGGAAGCCGAAGACAACACCCTGG 1620  Db  1561 TTGGACGGGGAAACTTTTGGCGAAGATGTTCAGCGGACGCCTGCAAGCCGAACAACACCCTGG 1620  OY  1621 TGGCGGTGAAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGG 1680  1621 TGGCGGTGAAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGG 1680  1681 AAGCGAGGATCCTGAAGCAGTACAGCCCCCAACATCGTGCGTCTCATTGGTGTCTGCA 1740		1261 1321 1321	Qy 1201 TGCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGGCCCCGGCGAGCCCC 1260	Oy 1081 AGCTCCGGAATGAAGGAGAACACCCCCGGGAGCGGGTGCAGCTGCCGAGGA 1140	1021 TGGCTGTGGCCACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGG	Qy 901 GTGTCACGTTCGATGAGTCACTGCTTGAGGAGGTGAACCGCTGGAGCTCC 960	QY 841 CTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCT 900	Qy 781 TGCAGGATGAGGTGGCCGATTCACCGGGAGATGGCTGCAGCTGCCGCCATCCAGC 840	Qy 721 AGGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGG 780	QY 661 ACCAGCACCACCACCAGCTCCTGCTGCCCGGCCTGCTGCGGTCACTGCAGGACCTGCACG 720	Qy 601 GGAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGGGGTGCGGGGTGCGCAGCTACACC 660

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           AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2674
                                                      ATGCAGCGCCGTGTCTCTCTGTGTCCCTGCTGCCAGGGCTTCCTCTTCCGGGCAGA
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RESULT 3
US-09-817-180-3
JS-09-817-180-3
JS-09-817-180
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Sequence 3, Application US/10003295

; Sequence 3, Application US/10003295

; Patent NO. 6686187

; GENERAL INFORMATION:
   APPLICANT: GAN, Weiniu et al.
   APPLICANT: GAN, Weiniu et al.
   TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTE
   TITLE OF INVENTION: THEREOF
   FILE REFERENCE: CL001183DIV
   CURRENT APPLICATION NUMBER: US/10/003,295
   CURRENT FILING DATE: 2001-12-06
   NUMBER OF SEQ ID NOS: 4
   SOFTWARE: FastSEQ for Windows Version 4.0
   SEQ ID NO 3
   LENGTH: 15297
   TYPE: DNA
   ORGANISM: Homo sapiens
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US-10-003-295-3
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTBINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001183
CURRENT FILING DATE: 2001-03-27
RUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15297
TYPE: DNA
ORGANISM: Human
                             Query Match
Best Local Similarity
Matches 363; Conserv
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Best Local Similarity 99.7
Matches 363; Conservative
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   2187 GGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAG
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                                  Conservative
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99.7%;
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99.7%;
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Pred. No. 5.1e-55;
0; Mismatches 1;
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                               Score 362.4; DB 4; pred. No. 5.1e-55; 0; Mismatches 1;
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Sequence 5, Application US/09387212A

Patent No. 6309849

GENERAL INFORMATION:
APPLICANT: ROBISON, KEITH E.
APPLICANT: ROBISON, WICLEIC ACID MOLECULES ENC.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENC.
FILE REFERENCE: MNI-0900

CUURRENT APPLICATION NUMBER: US/09/387,212A

CURRENT FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 18

SOPTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 361
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US-09-387-212-5
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US-09-387-212-5
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Best Local Similarity 97.4%;
Matches 333; Conservative
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                                                                                                                                            TCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAG
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ACTGCCTGGTGACAGAGAAGAATGTCCTGAAGAATCAGTGACTTTGGGGATGTCCCGAGA
                   ACTGCCTGGTGACAGAAGAAGAATGTCCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA 1981
                                                                                                  CTGCTGGCATGGAGTACCTGGAGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA
                                                                                                                                                                                 TCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAG
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Pred. No. 1.1e-43;
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RESULT 7
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US-09-948-802-5
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Best Local Simi:
Matches 333;
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CURRENT APPLICATION NUMBER: US/09/948,802
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 09/387,212
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09948802
Patent No. 6465232
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ROBISON, KEITH E.
TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 361
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Pred. No. 1.1e-43;
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Sequence 12110, Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03

APPLICATION NUMBER: 60/231,498

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; LENGTH: 19153
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15795
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows
SEQ ID NO 12110
LENGTH: 19152
TYPE: DNA
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Best Local Similarity 99.6
Matches 224; Conservative
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APPLICANT: VENTER, J.
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Patent No. 6812339
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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CGGGTCAAĜAGTGACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGT
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ilarity 99.6%;
Conservative
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Pred. No. 2.4e-30;
0; Mismatches 1;
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Pred. No. 2.4e-30;
0; Mismatches 1
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TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relate
TITLE OF INVENTION: Thereto
FILE REFERENCE: 2848-39
CURRENT APPLICATION NUMBER: US/09/814,915A
CURRENT APPLICATION NUMBER: 00/203-21
PRIOR APPLICATION NUMBER: 60/214,870
PRIOR FILING DATE: 2002-03-21
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.1
SEQ ID NO 82
US-09-814-915A-82
US-09-814-915A-82
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US-09-814-915A-82
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GENERAL INFORMATION:
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Best Local Similarity 54.7%;
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GGGAGGTGCTGAGCTTTGGGGACAAGCCTTATGGGGAGATGAGCAATCAGGAGGTTATGA
                                         GGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACACGG
                                                                                                                                               CCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTCT
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Jennifer
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Pred. No. 5e-26;
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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US-09-949-016-628
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SEQ ID NO 628
LENGTH: 3921
TYPE: DNA
ORGANISM: Human
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Best Local Similarity 55.1%;
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RESULT 11
US-09-949-016-2120
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US-09-949-016-2120
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Fatent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2120
LENGTH: 3921
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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AAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGG
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                                                                                                                 CGAGAGGAAGCCGATGGGGTCTATGCAGCCT---CAGGGGGCCTCAGACAAGTCCCCGTG
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PELLING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-31,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-5662
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307
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Best Local
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Patent No. 6812339
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CTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCC 1988
                                                                                                                                                                                                                                                              CGGAACAAGAACTCCCTGAAGGTGCTCACCCTCGTGCTGTACTCACTGCAGATATGCAAA 1682
                                                                                                                                                                                                                                                                                                                                                                                                                                   GAĞCCCACCTGGATCATCATGGAATTGTATCCCTATGGGGAGCTGGGCCACTACCTGGAG 1622
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Mismatches
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                                                                                         US-08-357-642A-2
    Query Match
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RESULT 13
US-08-357-642A-2
                                                                                                    Sequence 2, Application US/08357642A Patent No. 5837524
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PRODUCTS
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PATENT NO. JOYAGE PATENT NO. GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sima Lev
APPLICANT: Joseph Schlessinger
TITLE OF INVENTION: PYK2 RELATED
TITLE OF INVENTION: AND METHODS
TITLE OF SECUENCES: 16 TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440 APPLICATION NUMBER: US FILING DATE: December CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE: 1 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage SOFTWARE: Word Perfect CURRENT APPLICATION DATA: CORRESPONDENCE ADDRESS ATTORNEY/AGENT INFORMATION: OPERATING SYSTEM: IBM P.C.
COPERATING SYSTEM: IBM P.C.
COPERATING SYSTEM: IBM P.C.
COPERATING SYSTEM: ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth TYPE: nucleic acid CITY: Los Angeles STATE: California COUNTRY: ZIP: 90071-2066 LENGTH: linear December 15, nucleic single US/08/357,642A 2 Street 209/070 DOS 5.0

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Sequence 2, Application US/08460626
Patent No. 5837815
PATENT INFORMATION:
APPLICANT: SIMA LEV
APPLICANT: JOSEPH SCHLESSINGER
TITLE OF INVENTION: PYK-2 RELATED PRITITE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
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COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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US-08-460-626-2
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Best Local Similarity 54.7%;
Matches 392; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 3416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/35
FILING DATE: December 15,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPATIER: IBM Compatible
OPERATING SYSTEM: IBM P.C.
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08, FILING DATE: June 2, 1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 211/121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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    ATCGGGGTGCTGGAGAAAGGAGACCGGCTGCCCAAGCCTGATCTCTGTCCACCGGTCCTT
                                                                                                                        CTCTGGGAGACCTTCAGCCTGGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACA 2168
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                                  CGGGAGTTTGTGGAGAAGGGGGGCCGTCTGCCCTTGCCCCAGAGCTGTGTCTCTGATGCCGTG 2228
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Pred. No. 7.1e-22;
0; Mismatches 319;
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RESULT 14 US-08-460-626-2

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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016 474
FILING DATE: HERREUTE...
CLASSITET.
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Best Local Similarity 54.7%;
Matches 392; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: PRIOR APPLICATION NUMBER:
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TYPE: nucleic acid
STRANDEDNESS: single
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STATE: CALIFORNIA
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ATCATGAAGAACCTCGACCACCCGCACATCGTGAAGCTGATCGGCAT---CATTGAAGAG
                                                                  ATCCTGAAGCAGTACAGCCAACCCCAACATCGTGCGTCTCATTGGTGTTCTGCACCCAGAAG
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AW701492	BP256574	BQ924403	CK943999	BP332887	CK788677	BU191031	CK357411	AW130256	BQ712558	BQ679512	CA449888	CN298839	BM684264	BQ807439	BX381725	BY704806	BM922603	CV030188	BM929822	СВ990282
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ALIGNMENTS

## REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1 CR624741 LOCUS DEFINITION REFERENCE ORIGIN FEATURES COMMENT TITLE JOURNAL REMARK Query Match Best Local Similarity Matches 2205; Conserv TITLE JOURNAL AUTHORS source Web: www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invityogen. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F. Mammalia; Butheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 2461) Li.W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished 2461 bp mRNA line: full-length cDNA clone CS0DI069YK21 of Placenta of Homo sapiens (human). Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation CR624741.1 GI:50505548 HTC; CNSLT\_cDNA. Homo sapiens Genoscope Homo sapiens (human) (bases 1 to 2461) Conservative /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" /clone="CSODIO69YK21" /tissue\_type="Placenta Cot 2 /plasmid="pCMVSPORT\_6" Location/Qualifiers .2461 67.6**%**; 85.3**%**; 0; Score 1806.8; DB 3; Pred. No. 2.1e-311; 0; Mismatches 2; 25-normalized linear centa Cot Indels Length 2461; 377; Euteleostomi; HTC 21-JUL-2004 25-normalized Gaps 2;

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TCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAGGCCCTTAACTACGGC 2066	GAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCCGATGGGGTCTATGCAGCC 2006			TO AGARACTETECTGCAGATGGTGGGGGATGCAGCTGGCATGGAATACETGGAG 1886					CCATGAGGACCTGGTGTTGGGTGAGCAGATTGGACGGGGAACTTTGGCGAAGTG 1506	177			TGCTGTCGGTGCTGTGGGATGGTCTGCCCCGGCACTTCATCATCATCCAGGCTCACGC 1560	AGCTGCTGGTGCACTCTGGGGAACTTCCTGGTGCGGGAGCCAGGGCAAGCAGGA 1500	1390		CCACCGCTGCAGCTCATTCCGGA	GAGCAGGAGCGAGAGGGGGAAGGACACCCACGCTGGAGATCCTTAAGAGCCA 1320	CGGAGCAGGAGCGAGAGGGGGGAAGGACACCCACGCTGGAGATCCTTAAGAGCCA 1360	GCCCCGGCGAGCCCCGCCTGTGCTGCTCCTGCAGGATGACCGCCACTCCACGTC 1300	

Q B Q B Q B Q B Q B Q B Q B Q B Q B Q B	ORIGIN  Query Match Query Match Best Local Similarity 100.0%; Pred. No. 2.1e-201; Matches 1189; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1326 GGAAGGACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAG	ource	BP 191 91006 EVRY cedex - FRANCE (E-mail: - Web: www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-olig end enriched, double-strand cDNA was digest into the Not I and EcoR V sites of the pCMV was normalized. Library was constructed by division of Invitrogen.	com/ InVitroGe	Eukaryota; Metazoa; Chordata; Eukaryota; Metazoa; Primates; Mammalia; Eutheria; Primates; 1 (bases 1 to 1189) Li,W.B., Gruber,C., Jessee,J Full-length cDNA libraries and	CON full- cof Ho crs9 crs9 crs9 s HTC;	2307	Qy 2247 TGCTGGGCCTATGAGCCTGGGCAGCGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG	Qy 2187 GGGGCCGTCTGCCCCAGAGCTGTGCCCGATGCCGTGTTCAGGCTCATGGAGCAG	Qy 2127 CTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACACGGGAGTTTGTGGAGAAG	QY 2067 CGCTACTCCTCCGAAAGCGACGTGTGGAAGCTTTGGCATCTTGGCATCTTGGGAGACCTTCAGC	Db 2221 TCAGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAGGCCCTTAACTAC
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY
Email: segref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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BX356089 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI008YG07 5-PRIME, mRNA sequence.
BX356089
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1 (bases 1 to 936)
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                           CGGGGGAACTTTTGGCGAAGTGTTTCAGCGGACGCCTGCGAGCCGACAACACCCCTGGTGGCG
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/mol_type="mRNA"
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/clone="CSODIO08YG07"
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                                                                                                                                                    Mammalia, Butheria, Primates, Catarrhini, Homi

1 (bases 1 to 980)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 5, 2003 this sequence version replaced

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                               980 bp mRNA linear EST 08-API EX356088 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens Colone CSODI008YG07 3-PRIME, mRNA вепленге
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr. Web: www.genoscope.cns.fr
1st strand.cdnA was primed with a NotI-oligo(dT) primer. Five prime
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/clone_Tib="Yomo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional ann of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3373)
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M
                                                                                                                                                                                                                                                                                                                                                                      Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamato, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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3373 bp mRNA linear HTC 03-APH Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200003015 product:similar to PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FES/FPS (EC 2.7.1.112) (C-FES) [Mus
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                                                                                                                                                                                         The FANTOM Consortium and
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                                                                                                                                                                                                                                                                      The RIKEN Genome E FANTOM Consortium.
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Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Supploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-722 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, Fax:81-45-503-9216)

Please visit our web site (http://genome.gsc.riken.jp/) for further derails.
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                   AGCTGGAGCAGCGGCCCGACAGCCCTGTCAGCCAGTCCTGGGCAGAGATAACAAGCCAG
                                                  AGCCGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAA 308
                                                                                                                     AGTGA CAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Host: SOLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FES/FPS (EC 2.7.1.112) (C-FES) [Mus musculus] (SWISSPROT|P16879, evidence: FASTY, 77.2%ID, 100%length, match=3083)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J"
/db_xref="FANTOM_DB:1200003O15"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="lung"
/clone_Tib="RIKEN_full-length_enriched_mouse_cDNA_library"
/dev_stage="adult"
i. .3373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
/mol_type="mRNA"
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GCCAGAGCCGGGCCATCAGCCCTGA 268	208 CO	HANDICANGENGE COMPCTICE TO THE REFERENCE OF THE PROPERTY OF TH	73	1;	BM456755 LOCUS DEFINITION	into		O 6	?; Qy	Db	OPENING TO SEE T	pCMVSPORT 6 vector. Library Qy ructed by Life Technologies, a Db	I-oligo(GT) primer. Five prime Db digested with Not I and cloned	icage VERY cedex - FRANCE  OY  OFFICE OFFICE OFFI  OFFICE OFFI  OFFICE OFFI  O	replaced gi:30548660.		a; Vertebrata; Euteleostomi; ini; Hominidae; Homo. Qy	Qy Db	рь	936 DP mKNA IINGAY EST 24-MAK-2004 sapiens PLACENTA Homo sapiens cDNA clone CS0DE013YP02  geometre.		Qy	A 1408 QY	TCCTTAAAAGCCACÁTCTCAGGAAT 1372	GCATTCCACCTCCACGGAGCA 1488
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)	Contact: Robert Strausberg, Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.gc Tissue Procurement: ATCC CDNA Library Propararion.	ARS NIH-MGC http://mgc.nci.nih.gov/. S National Institutes of Health, Mammalian Gene Collection (MGC) AL Unnuhlished (1999)	Homo sapie M Homo sapie Eukaryota; Mammalia;	5', mRNA sequence. N BM456755 BM456755.1 GI:18505795 EST.	SS BM456755 1029 bp mRNA linear EST 05-FEB-2002 FION AGENCOURT_6403957 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583652	7		929 ACHSTRIGGGICHECHTSREGICERECTGIGTEREGIIEGAISBAIGHGICHETGGI 929 GGAGGGTGAAC 939	ACAGTATGGGTCCGCACCTGTGTCCACGTTCGATGAGTCACTGCTTGA	793 GGAGATGGCTGCAGCTGCCGGCATCCAGCCTGAGGCTGAGTACCAAGGCTTCCTGCG 852	809 GGAGATGGCTGCTGCCCGCATCCAGCCTGAGGCTGAGGTACCAAGGCTTCCTGCG 868	749 CCTGCAGGATACCTGGAGATTAGCAGCCTGGTGCAGGATGAGGTGGTGGCCATTCACCG 808		689 CGGCCTGCTGCGCTCACTGCAGGACCTGCACGAGGAGATGGCTTGCATCCTGAAGGAGAT 748	629 TGTGCTGGGGGGGGGGGGCAGCTACACCACCACCACCACCACCACCACCACCACCACCACC	CAAGGCCAAGGACAAGTATGTGCGCA-SCTGTGGAAGCTCTTTGCTCACACACCGCTA	569 CAAGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTTGCTCACCACAACCGCTA 628	509 ACGGGACAGTGCCCAAGCCAAGCGCAAGTACCAGGAGGCCAGCAAAGACAAGGACCGTGA 568		449 GCTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAGCCAGTACCGAGCTCTGGC 508	CGGGAACGGCAGCTTCGCAAGACCTACAGCGAGCAGTGGCAGCAGCTGCAGCAGGA	389 CCGGGAACGGCAGCTTCGCAAGACCTACAGCGAGCAGTGGCAGCAGCAGCAGCAGGA 448	329 GCTGCGGCAGAGAGGATCTGAACTCAGGGCCCCTGAGCAAGCTGAGCCTGCTCAT 388	269 CAGCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACTGAGGGCCTGAGCCGCTT 328	194 ACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGCCGGGCCATCAGCCCTGA 253

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/clone="IMAGE:5583652"

/tissue_type="embryonal carcinoma, cell line"

/tissue_type="embryonal carcinoma, cell line"

/tlone lib="NIH_MGC 92"

/clone lib="NIH_MGC 92"

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CCAGCACCACCACCAGCTCCTGCTGCCCGGNCTGCTGCGGTCACTGCAGGACCTGCACGA

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RESULT 8
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation
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Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 CGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAGCT
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                                                                                                                                                                                            32.3%; Score 863; DB 3; Le larity 100.0%; Pred. No. 2.3e-143; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/plasmid="pCMVSPORT_6"
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eliwas; Ito 989)

Eliwas; Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30376296.

Contact: Genoscope

Genoscope - Centre National de Sequencage

Genoscope - Centre National de 
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BX359009
BX359009.2 GI:46305682
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into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7663.f

For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO51BH10NP1&c=7663.f.

Location/Qualifiers
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source 1. 989

/ organism="Homo sapiens"
/mol\_type="mRNA"
/clone="CSODI051Y020"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone\_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone\_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
/primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

12 0%: Score 855 2: DR 5: Length 989:

1510 CCAAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGACGGG TGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACC-GGGACCTGGCTGGCTCGGAACT GCCGATGGGGTCTATGCAGCCTCAGGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCA 2045 CAGCCC-ATCTACATCGTCATGGAGCTTGTGCAGGGGGGGGACTTCCTGACCTTCCTCCG GAACTTTYGCGAAGTGTTCATGCGACGCCTGCGAGCCCAACAACAMCWCTGGTGGCGGTG GGAACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAACACC-CTGGTGGCGGTG CCAAAGAMAAGTGGGTS --TRACCATKAAGACCTGGTG-TGGGTGAGMARWTT-GACGG GTGTTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGC ACACGGGAGTTTGTGGAGAAGGGGGGCCGTCTGCCCCTGCCCAGAGCTGTGTCCTGATGCC TTGCTCTGGGAGACCTTCAGCCTGGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAG 335 TTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCCAACCTCAGCAATCAGCAG 2165 CCTGAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATC 2105 GCCGATGGGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCCCGTGAAGTGGACCGCA GCCTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTCCCCCMTGTCCCGAGAGGAGA GCCTGGTGACAGAGAAGAATGTCCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGA-A 1985 TGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCAGGGACCTGGCTCGGAACT CACGGAGGGGCCCG-CTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGC CACGGAGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGC CAGCCCAATCTACATCGTCATGGAGCTTGTGCAGGGGGGGCGACTTCCTGACCTTCCTCCG ATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAG ATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAG AAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGG ACACGGGAGTTTGTGGAGAAGGGGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCC Conservative GTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGG 32.0%; Score 855.2; DB 5; 95.8%; Pred. No. 5.6e-142; tive 14; Mismatches 18; Indels Length 9 Gaps 1628 275 2225 395 455 1926 1867 1807 1688 515 575 635 694 754 814 874 934 1569

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Matches 858; Conserv
                                                                                                                                                                                                                                                                                                                                                                           Li, W.B. Gruber, C. Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:30544306.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRY sites of the pcWVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 7663.f

This sequence belongs to sequence cluster 7663.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE004CGO5QP1&c=7663.f.
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AL540776 AL540776 AL540776.3 GI:45716373
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1. (bases 1 to 861)
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                                                                                                    Conservative
                                                                                                                                                                              /tissue_type="PLACENTA"
/clone_Tis="Homo sapiens PLACENTA"
/clone_Tis="Homo sapiens PLACENTA"
/note="Wector: pcfWVspOrT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned i
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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/clone="CSODE004YN09"
                                                                                                                  31.3%;
                                                                                               Score 836.6; DB 1;
Pred. No. 1.1e-138;
2; Mismatches 1;
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Bukaryota, Metazoa; Chordata; Craniata; Verteb Mammalla; Butheria; Primates; Catarrhini; Homi 1 (bases 1 to 968)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                              Homo sapiens (human)
                                                                                                                                                                                               968 bp mRNA linear ES BX359010 Homo sapiens PLACENTA COT 25-NORWALIZED Homo clone CS0DI051Y020 5-PRIME, mRNA sequence.
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                                                                                 Craniata; Vertebrata;
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqret@genoscope.cns.fr, Web: www.genoscope.cns.fr
let strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO51BH10QP1&c=7663.f. Location/Qualifiers
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TGGGCGTGCGGGCAGCTACACCACCAGCACCACCACCACCACCACCTGCTGCTGCCCGGCC
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                                                                                               CCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTTGCTCACCACAACCGCTATGTGC
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/db_xref="taxon:9606"
/clone="CS0DI051Y020"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
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1 (bases 1 to 848)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:30544304.

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime
1st strand cDNA was grimed with a NotI-Oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL540775 Homo sapiens PLACENTA Homo sapiens 3-PRIME, mRNA sequence.
AL540775 AL540775 AL540775 GI:45716372
                                                                                                                                                                                                                                                                                                                                                                                                  division of Invitrogen.

This sequence belongs to sequence cluster 7663.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CSODE004CGO5NP1&c=7663.f.
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                                                                                                           /tissue_type="PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/note="Vector: pcMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) prImer. Five prime end enriched,
double-strand cDNA was digested with Not I and conned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                  /clone="CS0DE004YN09"
                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/db_xref="taxon:9606"
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                         30.1%;
    Score 805; DB 1;
Pred. No. 4.8e-133;
1; Mismatches 15
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 939)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
                                                                                                                                                 BX381726 PARA PLACETTA COT 25-NORWALIZED HOMO ESTABLIZED HOMO ESTABLIZED HOMO CLONE CSODIO69YKZ1 5-PRIME, MRNA sequence.

BX381726
                                                                                 Homo sapiens
                                                                                                  Homo sapiens (human)
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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On May 8, 2003 this sequence version replaced
Contact: Genoscope
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      GCGGGCTGCGCAGCTACACCACCAGCACCAC-CACCAGCTCCTGCTGCCGGCCTGCTGC
                                                        CAAGTATGTGCGCAGCCTGTGGAAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGGCGT
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 913)
14.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:30606435.
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL569718 913 bp m
AL569718 Homo sapiens PLACENTA Homo
3-PRIME, mRNA sequence.
AL569718
AL569718 GI:46235981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                   For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODEO13DHO1NP1&c=7663.f. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence belongs to sequence cluster 7663.f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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                                                                  GGACGCCTGCGAGCCGACAACACCCTGGTGGCGGTGAAGTC-TTGTCGAGAGAGACGCTCCC
                                              GGACGCCTGCGAGCCRACAACACCCTGGTGGCGATGAAGTCTTTGTCGAGAGACGCTCCC
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                                                                                                                  Conservative
                                                                                                                                                                                                    /tissue_type="PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/note="Vector: pcfWySpORT 6; lst strand cDNA was primed
/note="Vector: pcfWySpORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned i
the Not I and EcoRV sites of the pcfWySpORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE013YP02"
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                                                                                                                29.6%; Score 791.6; DB 1; 94.5%; Pred. No. 1.2e-130; tive 17; Mismatches 27;
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sapiens cDNA clone CS0DE013YP02
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                                                                                                                                                                  5', mRNA sequence.
BQ708270
BQ708270.1 GI:2184
EST.
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Homo sapiens (human)
Homo sapiens
Edwaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae;
1 (bases 1 to 948)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                     948 bp
AGENCOURT_8484911 NIH_MGC_113 Homo
                                                                                                                                                                                                                                                                                                                                                 CTAGGTGCANCTCCTCAGCGGCTCCMGCHCATATGCTGACAGCTCTTCACAGTCCTGTAC 75
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Tissue Procurement: Dr. Mark Matson
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 610.
Location/Qualifiers
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     ATCCAGCCTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTC
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                                                                                                                                                       CTGCACGAGGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGC
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/clone_lib="NIH_MCC_113"
/clone_lib="NIH_MCC_113"
/clone_"Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: /note="Organ: spleen; Vector: poTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAe(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:6301278"
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Pred. No. 4.3e-127;
0; Mismatches 34;
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CCACCCTGTGTCACGTTCGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGG

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δ 문 Ş 밁 δ 묽 8

Search completed: March 19, Job time : 7733.14 secs

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Maximum DB
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Match
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Copyright (c) 1993 - 2005 Compugen Ltd.
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ADQ54298
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Aba94500 Human pro
Abv75413 Human kin
Adm28580 Human pro
Adk71888 Human kin
Aas95001 Human DNA
Adr39816 Human kin
Ada43980 CRAM prot
Aan70060 fes/fps p
Adl71052 Gene enco
Adq54298 Novel can
Abk84514 Human cDN
Aba94501 Human pro
Adw75414 Human kin
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Adl71054 Gene enco
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Adm361604 Human pro
Adm361604 Human pro
Abx14976 Human pro
Abx14976 Human pro
Abx14976 Human pro
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Human proto-oncogene tyrosine kinase encoding cDNA

09-APR-2002 (first entry)

ABA94500;

ABA94500 standard; cDNA; 2674 BP.

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185.4	185.4	185.4	185.4	185.4	185.4	185.4	185.4	185.4	198	198	198	198	198	198	198	198	198	198	199.2	199.6	201.2	201.2	271.6	271.6
6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.5	7.5	7.5	10.2	10.2
3921	3921	3921	3919	3346	3042	3042	3042	3042	3370	3370	3370	3370	3370	3370	2955	2955	2955	2955	2778	5616	3875	3286	3369	3198
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ADB37439	ABZ34865	ABV94231	ACN37278	ACN42099	ABL91659	ABX09937	ABZ35694	ABV78118	ADQ80244	ADJ75094	ADE38440	ADD18447	ABZ34861	ABL67952	ABL91658	ABX09936	ABZ35693	ABV78117	ADP28218	ADE08824	ABZ35414	ADK71885	ABL14457	ABL18403
Adb37439 Human can	Abz34865 Coding se	Abv94231 Breast ca	Acn37278 Tumour-as	Acn42099 Human dia	Abl91659 Human pol	Abx09937 Human eph	Abz35694 Human eph	Human		Adj75094 Marker ge	Ade38440 Human pro	Add18447 Human pro	Abz34861 Coding se	Ovary	Ab191658 Human pol	Abx09936 Human eph	Abz35693 Human eph	Abv78117 Human eph	Adp28218 Human sec	Ade08824 Novel DNA	Abz35414 Human gen	Adk71885 Human kin	Abl14457 Drosophil	Abl18403 Drosophil

## ALIGNMENTS

RESULT 1
ABA94
ABA94
XX ABA9
XX ABA9
XX Prot
XX CPT S'UT
FT CDS
FT CDS
FT CDS
FT 27-M
XX US63
XX US63 Proto-oncogene tyrosine kinase; poTK; tumour; cytostatic; anti-leukemic; gene therapy; protein therapy; vaccine; enzymatic-inhibition; human; anti-kinase; ss. Nucleic acids encoding a proto-oncogene tyrosine kinase, useful for the prevention, diagnosis and treatment of e.g. leukemia and lung tumors. WPI; 2002-138497/18. P-PSDB; ABB07354. Gan W, 3'UTR 5'UTR 27-MAR-2001; 2001US-00817180 27-MAR-2001; 2001US-00817180. 22-JAN-2002. US6340584-B1. Homo sapiens. (PEKE ) PE CORP NY. Ye J, Di Francesco /\*tag= a
72. .2330
/\*tag= b
/product= "proto-oncogene tyrosine kinase"
2331. .2674 Location/Qualifiers < Beasley EM;

8×333333333333333X&

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Query Match
Best Local Similarity
Matches 2674; Conserv
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                                                                       ACCAGCACCACCAGCTCCTGCTGCCCGGCCTGCTGCGGTCACTGCAGGACCTGCACG
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AGGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGG
                                                    ACCAGCACCACCAGCTCCTGCTGCCGGCCTGCTGCGGTCACTGCAGGACCTGCACG
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tive 0; Mismatches
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Human; kinase; proto-oncogene tyrosine kinase; antiarteriosclerotic; cytostatic; antiinflammatory; antipsoriatic; gene therapy; protein kinase; arug screening assay; tissue typing; chromosome 15; pharmacogenomic analysis; inflammation; cancer; leukaemia; lung tumours; kidney tumour; stomach adenocarcinoma; arteriosclerosis; psoriasis; gene;
                                                                                            Human kinase
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                                                                                                                                                                                                                  The invention relates to a newly isolated peptide sequence of a human CC kinase that is related to the proto-oncogene tyrosine kinase subfamily. CC The activity of the kinase of the invention may be described as, CC cytostatic, antiarteriosclerotic, antiinflammatory and antipsoriatic. CC Peptides of the invention are useful in assays to determine the CC biological activity of the protein, in drug screening assays, tissue CC diagnosing disorders characterised by an absence of, inappropriate, or CC diagnosing disorders characterised by an absence of, inappropriate, or CC unwanted expression of the protein, such as inflammation, cancer (e.g. CC leukaemia, lung tumours, kidney tumours or stomach adenocarcinoma), CC arteriosclerosis, and psoriasis. Nucleic acid molecules of the invention CC assays. The peptide and nucleic acid sequences are useful as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic targets, aid in the identification CC tissues that express the protein. The protein of the invention may also be useful in gene therapy. The gene encoding the protein may also be useful in gene therapy. The gene encoding the protein of the invention CC has been localised to human chromosome 15. The current sequence
                                                                                                                             Matches 2674;
                                                                                                                                            Query Match
Best Local Similarity
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5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human kinase protein, useful for treating or diagnosing disorders associated with an absence of, inappropriate, or unwanted expression of the protein, e.g. inflammation or cancer, in drug screening assays and pharmacogenomics.
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1201 TGCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGGCCCC 1260	1141 GGCAAGTGCTGCAAGAAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGGCCAGGCCAGGCCAAGC 1200	1081 AGCTCCGGAATGAAGAGGAGAACACCCACCCCGGGAGCGGGTGCAGCTGCTGGGCAAGA 1140	1021 TGGCTGTGGCCACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGG 1080	961 AGCTGAACGAGCTGACTGTGGAGAGCGTGCAGCACACGCTGACCTCAGTGACAGATGAGC 1020	901 GTGTCACGTTCGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGAGCTCC 960	841 CTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCT 900	781 TGCAGGATGAGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCCGCATCCAGC 840	721 AGGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGG 780	661 ACCAGCACCACCAGCTCCTGCTGCCGGCCTGCTGCGGTCACTGCAGGACCTGCACG 720	601 GGAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGGCGTGCGGGGCTGCGCAGCTACACC 660	541 AGGAGGCCAGCAAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGT 600	481 AGCTGAAGAGCCAGTACCGAGCTCTGĠCACGGGACAGTGCCCAAGCCAAG	421 GCGAGCAGTGGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGA 480	361 GGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACA 420	301 CCAGCCAAACTGAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAG 360 	241 GGGGCAGAGCCGGGCCATCAGCCCTGACAGCCCCATCAGTCAG	181 GGGTCAAGAGTGACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTG 240 181 GGGTCAAGAGTGACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTG 240	1 AGCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGC 18
р <u>(</u>	P &	- 5 B 2	\$ B &	}	?	P 5	P 5	₹ B \$	\$ \$ \$	5 B 2	P B 5	S B 2	5	S B 8	\$ B :	₹ <b>₽</b> ;	<b>₽</b>	δ
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06-DEC-2001;
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The invention relates to a new isolated human proto-oncogene tyrosine kinase peptide or its allelic variant, orthologue or fragment. The peptide is useful for preparing a composition for treating a disease or condition mediated by a human kinase protein e.g. cancer. The present
                                                                                         Claim 4; SEQ
                                                                                                                        New human kinase peptides, useful for preparing a treating a disease or condition mediated by human
                                                                                                                                                                              WPI; 2004-282461/26.
P-PSDB; ADM28581.
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ADK71888 standard; CDNA; 2599 ВÞ

ADK71888;

20-MAY-2004 (first entry)

Human kinase and phosphatase KPP-6 cDNA.

RESULT 4
ADK71888
ID ADK71888
ID ADK7
XX ADK7
XX ADK7
XX Huma
XX Huma human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic; hypotensive; vasotropic; antiaflamatory; antianginal; anti-HIV; antiallergic; antiasthmatic; immunosuppressive; antithyroid; dermatological; antidabetic; nephrotropic; antigout; gastrointestinal; neuroprotective; osteopathic; antiarthritic; uropathic; ophthalmological; antipsoriatic; hardisenian; nootropic; anticonvulsant; hepatotropic; antipsoriatic; hardisectoric; antipsoriatic; antibacterial; virucide; protozoacide; fungicide; cardiovascular disease; immune system; neurojatical; growth; development; cell proliferation; viral; bacterial; fungal; parastic; protozoan; halminthic infection; transgenic; gene therapy; ss; gene;

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Key variation Location/Qualifiers replace(109,T) /\*tag= a /label= Single nucle

a Single nucleotide polymorphism (SNP)

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The invention relates to a novel isolated polypeptide which is a human CC kinase and phosphatase (KPP). The polypeptide of the invention CC demonstrates cardiovascular, antiarterioscierotic, hypotensive, CC vasotropic, antianflammatory, antianginal, anti-HIV, antiallergic, CC antialsthmatic, immunosuppressive, antithyroid, dermatological, neuroprotective, antiatheritic, ophthalmological, antiparasitic, antiparasitic, antiparasitic, ophthalmological, antiparasitic, an
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Best Local Similarity
Matches 2537; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human kinases and phosphatases, useful for diagnosing, treating or preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
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25-SEP-2002; 2002US-0413910P.
27-SEP-2002; 2002US-0414296P.
11-OCT-2002; 2002US-0417821P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2599 BP;
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Matches 2558
                                                                                                                                                                                         The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as atheroselerosis, cerebral stroke, and cardiovascular disorders such as atheroselerosis, cerebral stroke, and cardiovascular disorders such as atheroselerosis. The polynucleotides sequences can also be used PCR primers and probes. The polynucleotides of the invention are also useful in gene therapy. As394746-AAS95021 represent the human polynucleotide sequences of the invention which are differentially expressed during foam cell differentiation
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Tai J;
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28-MAR-2003;
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2003US-0449059P.
2003US-0456932P.
2003US-0458844P.
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replace(109,C)
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CGAGCAGTGGCAGCAGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAA

264 301 305 361 305 421 421

GCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAG

205 242 265 302 306 306 306

CAGCCAAACTGAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAGG

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                                                                                                                                                                                                                                                                                                                                                                                                                   CC invention have cytostatic, antiarreriosclerotic, anticonvulent, conotropic, neuroprotective, cerebroprotective, anti-HTV, antiallargic, conotropic, neuroprotective, cerebroprotective, anti-HTV, antiallargic, cantiinflammatory and thyromimetic activities, and can be used in gene charapy. The human KPP proteins and polynucleotides can be used in continuous can be used in considered the decreased expression or overexpression of KPP, such as cell conferrative (e.g. cancer, atherosclerosis), neurological (e.g. AIDS, concer, atherosclerosis), neurological (e.g. AIDS, concer, atherosclerosis), neurological (e.g. AIDS, contents), and developmental (e.g. Hypothyroidism, Cushing's syndrome) conference of infections. They can also be used in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid compounds for effectiveness as agonist or antagonist of the polypeptides, cor in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide.
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Sim
Matches 2360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human kinases and phosphatases (KPP) for diagnosing, treating and preventing diseases or conditions associated with aberrant KPP expression e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ramkumar J, Marquis JP, Swarnaker A, Chawl
Becha SD, Lee SY, Hafalla AJA, Richardson
Jackson AA, Yang J, Gorvad AE;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2623 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-2003; 2003US-0461678P.
17-APR-2003; 2003US-0463937P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence encodes the human kinase and P), designated KPP-43. The human KPP sequences
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DB; ADR39770.
                                    182
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GGTCAAGAGTGACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGG
                                                                                                                                                                                  GAACAGCACTATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGGCCACGGGGTCCTGCA
                                                                                                                                                                                                                                                    CCGGGGTCCGCACCGGGCCTGAGTCGGTCCGAGGCCGTCCCAGGAGCAGCTGCCCGTGCG
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                                                                            GCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCG
                                                                                                                  GCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCG
                                                                                                                                                      GAACAGCACTATGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGCCACGGGTCCTGCA
                                                                                                                                                                                                                                CCGGGGTCCGCACCGGGCCTGAGTCGGTCCGAGGCCGTCCCAGGAGCAGCTGCCCGTGCG
                                  GGTCAAGAGTGACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGG
                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                        Score 1953; DB 13;
Pred. No. 1.5e-254;
0; Mismatches 5;
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1351 TGGGGACTTCCTGGTGCGGGAGAGCCAGGGCAAGCAGGAGTACGTGCTGTCGGTGCTGTG 1410		1291 GCAGCTGTGGTACCACGGGGCCATCCCGAGGGCAGAGGTGGCTGAGCTGCTGGTGCACTC 1350	1392 1391		11/1 GGGGGGAAGGACACCCACGCTGGAGAATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCC 1230 1382 CAAGTTCTCG 1391	GGGGGGAAGGACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCC	1262 GCCTGTGCTGCTGCAGGATGACCGCCACTCCACGTCGTCGTCGTGGAGCAGGAGCGAGA 1321	1202 GCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCCCC 1261	1142 GCAAGTGCTGCAAGAAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGGCCAGGCCAAGCT 1201	1082 GCTCCGGAATGAAGAGGAGAACACCCACCCCCGGGAGCGGGTGCAGCTGCTGGGCAAGAG 1141	1022 GGCTGTGGCCACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGGA 1081	962 GCTGAACGAGCTGAGCAGGAGCGTGCAGCACGCTGACCTCAGTGACAGATGAGCT 1021	902 TGTCACGTTCGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTCGGGGAGCTCCA 961	842 TGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCTG 901	782 GCAGGATGAGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCCGCCATCCAGCC 841	722 GGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGAGATTAGCAGCCTGGT 781	662 CCAGCACCACCAGCTCCTGCTGCCGGCCTGCGGTCACTGCAGGACCTGCACGA 721	602 GAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGGCGTGCGGGGCTGCGCAGCTACACCA 661	542 GGAGGCCAGCAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGTG 601	482 GCTGAAGAGCCAGTACCGAGCTCTGGCACGGACAGTGCCCAAAGCCAAAGCGAAGTACCA 541 
Ş	שלם	δ į	₽ 5	} B	S	<u> </u>	B 4	§	S B 1	S B 2	S B 2	§ § §	B &	? B &	dg dy	, B &	}	?	· 음 &	g dy
2432 CTGCCACCAGCATCCACACTGCCGGCAGGATGCAGCGCCGTGTCCTCTCTGTGTCCCTGC 2491	AGGTGCAGCTCCAGCGCTCCAGCTCATATGCTGACAGCTCTTCACAGTCCTGGACTC 2	AGGTGCAGCTCCTCAGCGCTCCAGCTCATATGCTGACAGCTCTTCACAGTCCTGGACTC	31.2   CUBARAGUSCATIUGSIBAGGUISGAACUUCUTIUUTUAAAGUISGAGGUUTUUGAGGUUT 23/1	GGCTTATGAGCCTGGGTATGTTTTTTTTTTTTTTTTTTT	2252 GGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGCACCATCTACCAAGGAGCTGCAGAGCAT 2311	2192 CCGTCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGAGCAGTGCTG 2251		CECCTOCCATABOUNCE OF USAGE 11 CONTROL OF THE CONTRO			GAAGATCAGTGAGCTTTTGGGATTGTCCCCGAGAGGAAGCTCGATGACAGTTCTATGCAGGCTCAGG	1892 GTGCTGCANTCCACCACTGCGTGCGTGCTGCAACATGCCTGCTGAGAGAAGAAGAATGCTTCTT 1891 1891 GAAGACTCTGCTGCAGATGGTGGGGGGATGCAGCTGCTGGCATGAAGAAGAAGCAA 1950		CARCATCOTGCCTCTCATTGGTCTCCACCCAGAAGCAGCCCATCTACATCGTCATGGA	ACCTGACCTCAAGGCCAAGTTTCTACAGGAAGGGAGGATCCTGAAGCAGTACAGCCACCC	Cosacce   Tolkasce   Casaca   Casaca	32 CCATGROSANC C 0931G I 1093 19A9CASA I 1GANCGOSGAACI I 1GANCAAGI 1G I CAG	72 CACCAAGAAGACTGSTESTTGTCCTGCACAGGGCTGTGCCCAAGGACAAGTGGGTGGG	GAAGGCTTTCCTAGCATTCCTTTGCTCATCGACCACCTACTGAGCACCCAGCAGCCCT	GATGGTCTGCCCCGGCACTTCATCCAGTCCTTGGATAACCTGTACCGACTGGAAGG

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RESULT 7
ADH43089
AD ADH4
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                                                                                                                                                                                 δ
                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 1970
                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for inducing neutralisation of cells or tissues by using a protein binding to CRAM (collapsing-response mediator protein-associated molecule) protein or its encoded gene. The proteins and their encoded genes are useful in gene therapy and regenerative medicine, e.g. by inducing neutralisation of mitochondria. They are also applicable in diagnosis, drug development for neural diseases and studying the mechanism of pathosis. The current sequence represents CRAM protein related cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genes and proteins participating in neutralization of cells or tissues, useful in gene therapy and regeneration medicine, applicable in discousies, drug development for neural diseases and study of mechanism
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P-PSDB; ADH43090.
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                                                                                                                                                                                                                                                                                                                                                    Sequence 2680 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; SEQ ID NO 1; 101pp; Japanese
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                                                                           CAGCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAG
                                                                                                                                                                   CGGAACAGCACTATGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTG
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                                                                                                                                                                                                                                                                                                                                                 629 A,
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                                                                                                                                                                                                                                                                                                                                                 758 C; 791
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                                                                                                                                                                                                                                         Score 1552.2; DB 12;
Pred. No. 1.6e-200;
0; Mismatches 303; 1
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                                                                                                                                 CTTCAGAGCTGTGCAGCCCCAGGGCCACGGGCAGTG
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                                                                                                                                                                                                                                                                                                                                                 502 T; 0 U;
                                                                                                                                                                                                                                            Indels 216;
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Query Match Best Local S Matches 856

al Similarity 856; Conser

32.0%; Score 856; DB 1; Lilarity 100.0%; Pred. No. 1.1e-106; Conservative 0; Mismatches 0;

Length 856; Indels

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Sequence 856 BP; 164 A; 265 C; 259 G; 168 T; 0 U; 0 Other;

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25-MAR-2003
27-JAN-1991
                      The fur gene, encoding furin, is in the human and cat genomes directly upstream of this fes/fps proto-oncogene sequence. Furin is strongly expressed in specific types of tunours and labelled RNA or DNA probes of the fur gene and antibodies against furin can be used for diagnostic purposes. (See also AAN70061-62 and AAP70056). (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                 Recombinant DNA contg. the fur gene - used for producing furin protand antibodies and as a diagnostic aid in the detection of tumours.
                                                                                                                                                                   WPI; 1987-328946/47.
P-PSDB; AAP70055.
                                                                                                            Disclosure; Fig 3; 24pp; English.
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(revised)
(first entry)
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Osteopathic; antiinflammatory; antirheumatic; antiarthritic; gene therapy; type II collagen; expression; cartilage disease; osteoarthritis; cartilage defect; rheumatoid arthritis; human;
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Matches 606;
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                                                      TGAGGAAGAGGAAGGACGAGCTGAAGCAGTTGGTGAGATTTTCCTTGGACGTTG
                                                                                                                                                            <u>AAAGACAGCCTGTCTACATCATTATGGAACTGGTCCCAGGGGGTGATTTTCTGACATTCC</u>
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cc significant portion of the canine genome. The isolated canine nucleic carid sequences of the invention may be useful for drug screening and coxicity assays. The invention is therefore useful for assessing the cimpact, including toxicity, of a compound; pharmaceutical agent or cell impact, including toxicity, of a compound; pharmaceutical agent or cell useful for detecting genes that are up- or down-regulated in canines in a ccl disease state. The sequences are useful as diagnostic agents or markers created to detect a cellular response in a sample individually or as part of a gene expression profile. It is also useful as target for agents that cell gene expression or activity. The database is useful for conducing electronic Northerns that allow the user to determine the cell type or tissue in which a given gene is expressed and to allow cell type or tissue or cell. The methods are useful for determining the similarity of a toxic response to one or more individual compounds. The similarity of a toxic response to one or more individual compounds. The cell itself hood that a compound or test agent will induce various specific pathologies such as those of the liver (liver necrosis, fatty liver cell broads are useful for mation or hepatitis), those of the kidney, the potential cellular pathways influenced, induced with at least one of the toxins. The methods are also useful for predicting or elucidating the compound or test agent due to the similarity of the expression profile compared to the profile induced by a known toxin. The present sequence is that of a canine DNA sequence which was claimed for use during the correduction of a canine microarray of the heating the during the
                                                             production of a canine microarray of the invention.
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Sequence 527 BP; 97 A; 157 C; 162 G; 98 T; 0 U; 13 Other;

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Best Local Similarity
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                          GGGACCCCTTCTCAAGCTGGTGGCCTCTGCAGGC 2369
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GGG-CCCCTTCTCAAGCTGGAGGCCTCTGTGGGC 454
                                                       CCAGCTTCNNNNNNNNNNNTACCAGNNGCTGCAGAGCATCCGGAGGCGGCATCGGTGAGGCT
                                                                                     CCAGCTTCAGCACCATCTACCAGGAGCTGCAGAGCATCCGAAAAGCGGCATCGGTGAGGCT
                                                                                                                                   GTCCTGATGCCGTGTTCAGGCTCATGGAGCAGTGCTGGGGCTATGAGCCTGGGCAGCGGC
                                                                                                                                                                           GCAATCAGCAGACCCGGGAGTTTGTGGAAAAAGGGGGGCCGCCTGCCCTGCCCAGAGCTGT
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89.2%;
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Pred. No. 1e-41;
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This invention is related to a novel isolated canine nucleic acid sequences and the construction of canine microarrays containing a

RESULT 11
ABK84514
ID ABK84
XX
AC ABK84
XX
AC ABK84
XX
DT 14-AU

ABK84514 standard;

CDNA; 12263

₽P

14-AUG-2002 ABK84514;

(first entry)

Human cDNA differentially expressed in granulocytic cells #1085

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CC DNA chip analysis as given in the specification, and comparing the capression level to an expression level in an unactivated GC, where CC differential expression of Gs is indicative of GcA. Also included are CC differential expression of Gs is indicative of GcA. Also included are CC expression of at least one gene in Gs; (2) screening (M3) for an agent chart alters the CC expression of at least one gene in Gs; (2) screening (M3) for an agent classe, an allergic response in a subject, exposure of a subject tissue, an allergic response in a subject, exposure of a subject to a profile; (3) detecting (M4) an inflammation (especially chronic) in a CC pathogen or sterile inflammatory disease, by detecting the level of comparison of the gene is indicative of inflammation; (4) treating CC exposures on of the gene is indicative of inflammation; (4) treating CC exposures in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression of the gene is indicative of inflammation; (4) treating CC exposure of a subject, exposure of a subject to a pathogen or sterile inflammation of the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M3 is useful for modulating GA; M3 is useful CC exposure of a subject to a pathogen or sterile inflammation with an inflammatory disease (e.g. cardiac reperfusion injury, renal reperfusion injury, ARDS, adult CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g. cardiac reperfusion inflection, parasitic infection, protozoal infection, con pathogen infection, protozoal infection, con pathogen infection, trial infection, parasitic infection, protozoal infection, con pathogen in a gene captured and specification. But was obtained in
    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2000; 2000US-0237189P
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                                                                                            Sequence 12263 BP; 2497 A; 3568 C; 3664 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENE-) GENE LOGIC INC.
                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                     form part of the printed specification, stronic format directly from WIPO at
13.6%;
    Score 362.4;
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    BG
                                                                                            2534 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                      but was obtained in
6; Length 12263;
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Matches 363; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                ABA94501;
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         exon
                                                                                                                                                                                                                                                                                                           anti-kinase; ds.
                                                                                                                                                                                                                                                                                                                   Proto-oncogene tyrosine kinase; poTK; tumour; cytostatic; anti-leukemic; gene therapy; protein therapy; vaccine; enzymatic-inhibition; human;
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Best Local Similarity 99.7
Matches 363; Conservative
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oncogene tyrosine kinase (poTK). The poTK polynucleotides and protein may
be used in the prevention, diagnosis and treatment of diseases associated
with inappropriate poTK expression, such as lung and kidney tumours,
leukemia and stomach adenocarcinoma. poTK may be used to treat disorders
associated with decreased expression by rectifying mutations or deletions
in a patient's genome that affect the activity of poTK by expressing
inactive proteins or to supplement the patients own production of poTK.
The encoded poTK may be used as an antigen in the production of
antibodies against poTK and in assays to identify modulators of poTK
expression and activity. The anti-poTK antibodies and antagonists may be
used to down regulate expression and activity and as diagnostic agents
for detecting the presence of poTK in samples. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding a proto-oncogene tyrosine kinase, useful for the prevention, diagnosis and treatment of e.g. leukemia and lung tumors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 3A-G; 49pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represents the human poTK genomic DNA sequence
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P-PSDB; ABB07354.
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2547 AAAA 2550
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                                                                                                         GACTCCTGCCACCAGCACCACCACTGCCGCAGCAGGATGCAGCGCCGTGTCCTCTGTGTC 1323:
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                                                                                                                                                                                                                                                                          AGCATCCGAAAGCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCA
                                                          CCTGCTGCTGCCAGGGCTTCCTCTTCCGGGCAGAAACAATAAAACCACTTGTGCCCACTG 2546
                                                                                                                                         GACTCCTGCCACCAGCATCCACACTGCCGGCAGGATGCAGCGCCGTGTCCTCTGTGTC
                                                                                                                                                                                 GGCCTAGGTGCAGCTCCTCAGCGGCTCCAGCTCATATGCTGACAGCTCTTCACAGTCCTG
                                                                                                                                                                                                                                                       AGCATCCGAAAGCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCA
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                                     CCTGCTGCTGCCAGGGCTTCCTCTTCCGGGCAGAAACAATAAAACCACTTGTGCCCACTG 1329
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/number= 16
12939. .13078
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intron

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exon

number= 9

exon

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intron

exon

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exon

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number= 4

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exon

9634. .10229 /\*tag= w /number= 11 10230. .10348 /\*tag= x /number= 12

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ARBSULT 13
ABV75414
ID ABV75414
ABV7541
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2563. .2775
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776. .2927
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7924. 8007
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7362. .7484

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number= 4
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                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a newly isolated peptide sequence of a human CK kinase that is related to the proto-oncogene tyrosine kinase subfamily. The activity of the kinase of the invention may be described as, compared to the proto-oncogene tyrosine kinase subfamily. The activity of the kinase of the invention may be described as, compared to the invention are useful in assays to determine the compared to the invention are useful in assays to determine the compared to the invention are useful in drug screening assays, tissue compared to the invention are useful in treating or disorders characterised by an absence of, inappropriate, or compared to the protein, such as inflammation, cancer (e.g. compared to the protein, such as inflammation, cancer (e.g. compared to the protein, such as inflammation, cancer (e.g. compared to the protein, such as inflammation, cancer (e.g. compared to the protein, such as inflammation, cancer (e.g. compared to the protein and molecules of the invention as models for the development of human therapeutic targets, and in the identification compared to the protein and serve as targets for the development of human characteristic for the invention may also be useful in gene therapy. The gene encoding the protein of the invention compared to human characteristic may also be useful as the human characteristic may also be useful as the human characteristic may also be useful to human characteristic may also be useful as the human characteristic may be useful as the human characteristic may be useful as a new part of the human characteristic ma
                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 363; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human kinase protein, useful for treating or diagnosing disorders associated with an absence of, inappropriate, or unwanted expression of the protein, e.g. inflammation or cancer, in drug screening assays and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-2001; 2001US-00817180.
06-DEC-2001; 2001US-00003295.
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                                                                                                                                                                                                                                                                                                                                                                   represents the human kinase genomic DNA sequence
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AGCATCCGAAAGCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCA 2366
                                               TGCTGGGCCTATGAGCCTGGGCAGCGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG
                                                                                                                                       GGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAG
                                                                              TGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG
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/number= 17
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/number= 16
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/*tag= aq
/number= 16
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11335. .11458
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number= 15
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                                                                                                                                                                                                                                Score 362.4; DB 8;
Pred. No. 3.6e-40;
0; Mismatches 1;
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RESULT 14
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                                                                                                                                   /*tag= i
/note= "Single nucleotide
replace(2808,t)
                             replace (4312,t)
                                                                                                     /note= "Single nucleotide polymorphism'
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replace(2484,t)
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replace(2159,c)
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replace(847,g)
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                                                                    note= "Single nucleotide polymorphism"
1928. .3101
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/note= "Single nucleotide polymorphism"
2776. .2927
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Best Local Similarity 99.7%;
Matches 363; Conservative
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                                  Osteopathic; antiinflammatory; antirheumatic; antiarthritic; gene therapy; type II collagen; expression; cartilage disease; osteoarthritis; cartilage defect; rheumatoid arthritis; human;
                                                                                                          Gene encoding type II collagen expression promoting protein, seq
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Pred. No. 3.6e-40;
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Matches 573;
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19-APR-2002; 2002US-0373594P
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CTGGTAGGTGAAAATAATGTTCTGAAAATCAGTGACTTTGGAATGTCTCGTCAAGAGGAT
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                                                                                                                                                                                                                                             GAAGCTCTTAATTATGGGAGATACAGTTCAGAGAGTGACGTGTGGAGCTTTGGCATCCTT
                                                                                                                                                                                                                                                             GAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAAGCGACGTGTGGAGCTTTGGCATCTTG
                                                                                                                                                                                                                                                                                                                               GATGGGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCCCGTGAAGTGGACCGCACCT
CTTCAGAAAGAGCTCACTATCATC
                                                                                                                     AGAGAGCAAGTAGAAAGAGGATACCGGATGTCAGCTCCCCAGCACTGTCCAGAGGATATT
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                                                          TCCAAAATCATGATGAAGTGTTGGGATTATAAACCTGAAAATCGCCCTAAGTTCAGTGAA
                                                                                       TTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGGCAGCGGCCCAGCTTCAGCACC
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Search completed: March 19, 2005, 04:31:15 Job time : 1290.71 secs This Page Blank (uspto)

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Result
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198	198	201.2	221.8	221.8	230.6	266.8	268.4	271.6	271.6	271.6	274.4	296.2	296.2	318.4	328.8	342.8	362.4	362.4	362.4	362.4	362.4	362.4	374.8	375	376.6
7.4	7.4	7.5	8.3	8.3	8. 6	•	10.0	10.2	10.2	10.2	10.3	11.1	11.1	11.9	12.3	12.8	13.6	13.6	13.6	13.6	13.6	13.6	14.0	14.0	14.1
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CQ776660 Sequence	AX481387 Sequence	Z27409 H.sapiens m	E01406 DNA sequenc	A06936 H.sapiens f	CQ726604 Sequence	X52844 Drosophila	U50450 Drosophila	BT003462 Drosophil	CQ591168 Sequence		AB006567 Ephydatia	AR236724 Sequence	AR175607 Sequence	Y17051 Sycon rapha	J03358 Human tyros	AF187884 Canis fam	AC004586 Homo sapi	AC124248 Homo sapi	AC003004 Human Chr	AR456324 Sequence	AR183262 Sequence	X06292 Human c-fes	X13412 Rat mRNA fo	M32054 Mouse tyros	U76762 Mus musculu

## ALIGNMENTS

RESULT 1

AR183261 LOCUS LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	2674 bp US 634058 4 4 cesco, V. a proteins,
JOURNAL FEATURES SOURCE	, and uses thereof 1 22-JAN-2002; 11fiers nknown"
Query Match Best Local Sig Matches 2674;	Query Match 100.0%; Score 2674; DB 6; Length 2674; Best Local Similarity 100.0%; Pred. No. 0; Matches 2674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
B &	1 TCCGGGGTCCGCACCGGGCCTGAGTCGGTCCGAGGCCGTCCCAGGAGCAGCTGCCCGTGC 60 1 TCCGGGGGTCCGCACCGGGCCTGAGTCGGTCCGAGGCCGTCCCAGGAGCAGCTGCCCGTGC 60
γ	GGAACAGCACTATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCCACGGGGTCCTGC
	GGAACAGCACTATISGGCTTCTCTTCTGAGCTGTGCAGCCCCAGGGCCACGGGGTCCTGC
Db 1	121 AGCAAATGCAGGAGGCCGAGCTTCGTCTACTCGAGGGGCATGAGAAAGTGGCCCAGC 180 
. 8	181 GGGTCAAGAGTGACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGGTG 240
Qy 2	241 GGGGCCAGAGCCGGGCCATCAGCCCTGACAGCCCCATCAGTCAG

QY 2401 TATGCTGACAGCTCTTCACAGTCCTGGACTCCTGCCACCAGCATCCACACTGCCGGCAGG	CGCC 1	1321 AGGGGGAAGGACACCCA	
2341 C 2341 C	GCCTGTGCTGCTGCAGGATGACCGCCACTCCACGTCGTCCTCGGAGCAGGAGCGAG 1320	1261 CGCCTGTGCTGCTGC.	
2281	TGCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCCC 1260	1201 TGCAGGCCCAGCAGGAGT	
2221 F	GGCAAGTGCTGCAAGAAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGCCAAGCCAAGC 1200	1141 GGCAAGTGCTGCAAGAAG	
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Qy 2101 GCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATC			
Qy 2041 CCGCACCTGAAGCCCTTAACTACGGCCGCTACTCCTCCGAAAAGCGACGTGTGGAGCTTTG	9AGC 1		
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Qy 1921 GGAACTGCCTGGTGACAGAGAAGANTGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAG 	CTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCT 900		
0-0	GAGATGGCTGCAGCTGCCCGCATCCAGC 8	TGCAGGATGAGGT	
Oy 1801 TCCTCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGATG	AGGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGG 780	<b>D</b> —D	
1741 C	()—()	<b>2</b> —2	
1681 A	CTTTGCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCGCAGCTACACC 660	601 GGAAGCTCTTTGCTCACC	
1621 1	AGGAGGCCAGCAAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGT 600	541 AGGAGGCCAGCAAAGACAJ             541 AGGAGGCCAGCAAAGACAJ	
1561 1	AGCTGAAGAGCCAGTACCGAAGCTCTGGCACGGGACAGTGCCCAAGCCGAAGTACC 540	481 AGCTGAAGAGCCAGTACCC	
1501 0	TGGCAGCAGCTGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGA 480	421 GCGAGCAGTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	
1 14 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	GGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACA 420	361 GGCCCCTGAGCAAGCTGAG	
1381	CAGCCAAACTGAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAG 360	301 CCAGCCAAACTGAGGGCC	
Db 1321 AGGGGGGAAGGACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCC			

OY 421 GCGAGCAGTGGCAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGA 480	QY 361 GGCCCCTGAGCAAGCTGAGCCTGATCCGGGAACGGCAGCAGCAGCTGCAAGACCTACA 420	QY 301 CCAGCCAAACTGAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAG 360	QY 241 GGGGCCAGAGCCGGGCCATCAGCCCCTGACAGTCAGTCAG	OY 181 GGGTCAAGAGTGACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTG 240	QY 121 AGCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGC 180	61 GGAACAGCACTATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGC	Qy 1 TCCGGGGTCCGCACCGGGCCTGAGTCGGTCCCAGGAGCAGCAGCTGCCGTGC 60	Query Match 100.0%; Score 2674; DB 6; Length 2674; Best Local Similarity 100.0%; Pred. No. 0; Matches 2674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Bource	Isolated human kinase proteins, nucleic acid human kinase proteins, and uses thereof Patent: US 6686187-A 1 03-FEB-2004; Location/Oualiflers	NISM Unknown.  Unclassified.  1 (bases 1 to 2674)  DRS Gan.W. Ye.J. Di Francesco.V.	GI:42691378	AR456323	641 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		2521 AACAATAAAACCACTTGTGCCCACTGAAAAAAAAAAAAA		OY 2461 ATGCAGCGCCGTGTCCTCTGTGTCCCTGCTGCTGCCAGGGCTTCCTCTTCCGGGCAGA 2520
OY 1501 GGCTGTGCCCAAGGACAAGTGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGA 1560 Db 1501 GGGCTGTGCCCAAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGA 1560	1441 TCGACCACCTACTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGGTGTTGTCCTGCACA 15	1381 CCAAGTTCTCGAACCTGTACCGACTGGAAGGGGAAGGCTTTCCTAGCATTCCTTTGCTCA	1321	1261 GGCTGTGCTGCTGCAGGATGACCGCCACTCCACGTCCTCGAGCAGAGCGAGC	1201 TGCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCCCC  1201 TGCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCCC	1141 GCCAAGTCCTGCAAGCACCTGCAAGGCCTGCAAGCCGAGCCCAAGCCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGAAAAAA	OY 1081 AGCTCCGGAATGAAGAAGAACACCCACCCCGGGAGCGGGTGCAGCTGCTGGGCAAGA 1140 Db 1081 AGCTCCGGAATGAAGAAGAACACCCACCCCCGGGAGCGGGTGCAGCTGCTGGGCAAGA 1140	TGGCTGTGGCCACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGG	AGCTGAACGAGCTGACTGTGGAGAGCGTGCAGCACACGCTGACCTCAGTGACAGATGAGC	Oy 901 GTGTCACGTTCGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGGCTGC 960	QY 841 CTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCT 900	Oy 781 TGCAGGATGAGGTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCCCGCATCCAGC 840	Qy 721 AGGAGATGGCTTGCATCCTGAAGGAGATTACCTGGAGATTAGCAGCCTGG 780	Qy 661 ACCAGCACCACCAGCTGCTGCTGCTGCTGCGGTCACTGCAGGACCTGCACG 720	Qy 601 GGAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGGCGTGCGGGGTGCGCAGCTACACC 660	Qy 541 AGGAGGCCAGCAAAGACAAGGACCAAGGCCAAGGACAAGTATGTGCGCAGCCTGT 600	Qy 481 AGCTGAAGAGCCAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCGAAGTACC 540	Db 421 GCGAGCAGTGGCAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGGCCAGGACATTGAGA 480

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Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsleh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gbbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Kodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Boutferd, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and intilal analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 51 Row: e Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 133769
                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
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Submitted (31-JUL-2002) National Institutes of Health, Mammalian Submitted (ollection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/organism="Homo sapiens"
/mal_type="mRNA"
/db xrefe="taxon:5606"
/clone="MGC:34142 IMAGE:5170548"
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Best Local Similarity 92.5%;
Matches 2576; Conservative
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GCTGAAGAGCCAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCCAAGCGCAAGTACCA
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AGLLHHMSLODSGGGSRAISPDSPISOSWAEITSQTEGLEKLLEQHAEDLNSGFLSKL
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KDKDRDKAKDKYVRSLWKLFAHHNRYVLGVRAAQLHHQHHHQLLHGLLRSLQDLHEE
MACIIKEILQEYLEISSLVQDEVVAIHREMAAAARIQEBAYQFLRQYGSAPDVPP
CVTFDESLLEEGEPLEFGELQLMEITVESVQHTLTSVTDELAVATEMVPRRQEMVYQL
QQELRNEEENTHPRERVQLLGKRQVLQBALQGLQVALCSQAKLQAQGELQTKLEHLG
PGEPPPVLLLQDDRHSTSSSEQEREGGRTPTLEILKSHISGIFRPKFSLPPPLQLIPE
VQKPLHEQLWYHGAIPRAEVAELLVHSGDFLVRESQGKQFVLSVUMDGLPRHFIIQS
LDNLYRLEGEGEPSIPLIDHLSTQOPLTKKSGVYLLSVUMDGLPRHFIIQS
LDNLYRLEGEGEPSIPLIDHLSTQOPLTKKSGVYLHBAVPKDKWLNHEBDLVLGEQ
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VCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTLLGWYGDAAAGMEYLLESKCCHR
DLAARNCLYTEKUVLKISDFGMSREEAADGVYAASGGGLRQVPVKWTAPEALNYGRYSSE
SDVWSFGILLMETFSLGASPYPNLSNQQTREFVEKGGRLPCPELCDDAVFRLMEQCWA
YEPGQRPSFSTIYQELQSIRKRHR"
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/product="V-FES feline sarcoma viral/V-FPS fujinami avian sarcoma viral oncogene homolog"
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/db_xref="GI:23271525"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Brain, adult medulla"
/clone_lib="NIH_MGC_119"
/lab_host="DH10B"
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/db_xref="LocusID:2242"
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CTGCCACCAGCATCCACACTGCCGGCAGGATGCAGCGCCGTGTCCTCTCTGTGTCCCTGC
                                                             AGGTGCAGCTCCTCAGCGCTCCAGCTCATATGCTGACAGCTCTTCACAGTCCTGGACTC
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H. sapiens RNA for c-fes.
X52192.1 GI:29890
fes cellular oncogene.
Homo sapiens (human)
Homo sapiens
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1 (bases 1 to 2771)

Alcalay,M., Antolini,F., Van de Ven,W.J., Lanfrancone,L., Grignani,F. and Pelicci,P.G.
Characterization of human and mouse c-fes cDNA clones and identification of the 5' end of the gene
Oncogene 5 (3), 267-275 (1990)
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 GAACAGCACTATGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCA
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Genes expressed in foam cell differentiation
Patent: WO 0177389-A 256 18-OCT-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNA"
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                                                                                          62 GAACAGCACTATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGGCCACGGGGTCCTGCA
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                                                                                                                                                                                                                       Patent: WO 02068579-A 11154 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
1. .2697
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                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                  GCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCG
GGTCAAGAGTGACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGG
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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1021 GCTCCGGAATGAAGAGAGACACCCACCCCGGGAGGCTGCAGCTGCTGGGCAAGAG 11021 GCTCCGGAATGAAGAGGAGAACACCCACCCCCGGGAGGGGTGCAGCTGCTGGGCAAGAG 11021 GCTCCGGAATGAAGAGGAGAACACCCACCCCCGGAGGCGAGCGGGTGCAGCTGCTGGGCAAGAG 1103 GCAAGTGCTGCAAGAAGAACACCCACCCCCCGGAGGCGAGCCTGTGCAGCCAAGCT 1104 GCAAGTGCTGCAAGAAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGCCAGGCCAAGCT 1105 GCAAGTGCTGCAAGAAGCACTGCAGGGGCTGCAGGTAGCCCCGGCGAGCCCCC 1207 GCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTTGAGCACCTGGGCCCCGGCGAGCCCCC 1107 GCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTTGAGCACCCCCCCC	2 TGTCACGTTCGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTCGAGGAGCTCCA 9	722 GGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGAGTACCTGGAGATTAGCAGCCTGGT 781	601 CCAGCACCACCACCACCACCTCCTGCTGCCCTGCTGCGGTCACTGCAGGACCTGCACGA	22 CGAGCAGTGGCAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAA 4	121 GGTCAAGAGTGACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTTGG 180 242 GGGCCAGAGCCGGGCCATCAGCCCCTGACAGGCCCATCAGTCCTGGGCTGAGATCAC 301
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2101 GARGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCCGATGGGGGTCTATGCAGCCCTCAGG 2160 2012 GGGCCTCAGACAAGTCCCCGTGAAGTGGACCCGCAGCCCTTAACTACGGCCGCTA 2071	1772 GCTTGTGCAGGGGGCGACTTCCTGACCTTCCTCCGCACGGAGGGGCCCGCCTGCGGGT 1831	1741 CGGACGCCTGCGAGGCCGACAACACCCCTGGTGGCGGTGAAGGCCTTGTTGTCGAGAGACGCCCCC 1800  1652 ACCTGACCTCCAAGGCCAAGTTTCTACAGGAAGACGCGAGGATCCTGAAGCAGTACAGCCACCC 1711	1561 GGANGGCTTCCTAGCATACCACCACCTGGCGGGGAAGTCTTCGCGAGAGAGCCCCCC 1620  1472 CACCAAGAAGAGTGGTGTTGTCCTTGCCACAGGCCCCAAGGACAAGTGGGTGCTGAA 1531	1392  1441 TGGGGACTTCCTGGTGCGGGAAGCCAGGGCAAGCAGGAGTACGTGCTGTCCGTGTCTGTG 1500  1392AACCTGTACCGACTGGAAGG 1411  1392	GGGGGAAGGACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCC

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Wilks,A.F. and Kurban,R.R.
Isolation and Structural analysis of murine c-fes cDNA clones Oncogene 3 (3), 289-294 (1988)
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                                               SVLIRERHSLEKTYNEOMOGLOGELTKTHSODIEKLKTOYKTLVRDSTOARRKYQEAS
KOKORDKAKOKYVRSLMKLFAHHRYVLGVRAAQLHHHHHRYPLLGELLOSLODLHEE
MAGILKDILGEYLE ISSLVQDDVAS IHRELAAAARIQEEFEYLGELROYSTPDVPP
CVTFDSSLLEDGEQLEPGELQLMELTLESVQHTLTSVTDELAVATKEVLSRGMYSQL
QRELQSERQNTHPRERVQLLSKRQMLQEAIQGLOIALCSQDKLQAQQELLQSKMEQLG
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KPLYEQLWYHGAIPMAEVAELLTHTGDFLVRESQGKQEYVLSVMMDGHPRHFIIQSLD
NLYRLEGDGFPSIPLLITHLLSSQQPLTKKSGVVLFRAVPKDKWVLKHEDLVLGEQIG
RGNFGSVFSGRLRADNTPVAVKSCRETLPDLKAKFQMAILKQYNHPNIVRLIGVC
TQKQPIYIVMELVQGGPFLTFLRTEGARLVKTTLQMGDAAAGMYLSKSCCIHRDL
AARNCLVTEKUVLKISDFGMSREEADGIYAACSGLRQVPKWTAPEALNYCRYSSESD
VMSFGILLMETTFSLGASPYPNLTNQOTREFVEKGHRLPCPELCDDAVFRLMEQCWAYE
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/db_xref="UniProt/Swiss-Prot:P16879"
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone_lib="lambda gt11.
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Fujinami sarcoma virus
Fujinami sarcoma virus
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
I (bases 1 to 2715)
S (Chen,L.H., Hatada,B., Wheatley,W. and Lee,W.H.
Single amino acid substitution, from Glui025 to Asp, of the oncogenic protein causes temperature sensitivity in transfo and kinase activity
Virology 155 (1), 106-119 (1986)
E 87044080
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M14930
M14930.1 GI:209688
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Original source text: Fujinami sarcoma integrated
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LSQTILRRHAEELAAGFLAKLSILIRDKQQLRKVFSEQWQQLSQEYAWTTQQEVEKLKA
LSQTERTHAEELAAGFLAKLSILIRDKQQLRKVFSEQWQQLSQEYAWTTQQEVEKLKA
QYRRLVRDSTQAKRKYQEASKDKEREKAKEKYVRSLGKYLYALHNQYVLAVQAAALHHR
HHYQRALFTLHESLYSLQQEMVLVLKEILGEYCSITSLVQEDVLAIHQVAHAVEMID
PATEYSSFVQCHRYDSEVPPANTFDESILEBAESLEFGELQLWELTIESVQHSLTSIE
EELLASRKAVSSKEQRWELQVELRGEELALSFGERWHLGKRQGLRERAQQLQGLVC
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YVLSVLWGQQPRHFIIQAADNLYRLEDDGLCTIPLLIDHLJOSQRFTTRKSGTVLTRA
VLKNKWVLAHBEDVLLGERIGRGNFGCTYNELDGGLFLASNTSLERBELSFRLYFELYAKFLQ
DARHLKQCCHHPNIVELIGVCTQKQPTYIVMELVQGGDFLSFLRSKGFRLXMKKLIXMM
DNAAAGMEYLESKHCIHRDLAARNCLVTEKNTLKISDFGWSRQEEDGYASTGGMKQI
DNAAAGMEYLESKHCIHRDLAARNCLVTEKNTLKISDFGWSRQEEDGYASTGGMKQI
DNAAAGMEYLESKHCIHRDLAARNCLVTEKNTLKISDFGWSRQEEDGYASTGGMKQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from ts FL-15.
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Fujinami Barcoma
/mol_type="genomic RNA"
/db_xref="taxon:11885"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                      /protein_id="AAA42403.1"
/db_xref="GI:209689"
                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                       /note="p140 transforming
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Duery Match  38.31, Score 1024.8, DB 14, Length 2715;  888.11.82   Soint 1024.8, DB 14, Length 2715;  888.12.82   Soint 1024.83   DB 14, Length 2715;  888.12.82   DB 14, Length 2715;  888.12.83   DB 14, Length 2715;  888.12.83   DB 14, Length 2715;  888.12.84   DB 14, Length 2715;  889.12.84   DB 14, Length 2715;  89	
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8	
1175 AGANGMAGCTOTTGGCCAGCAGAMAGCACTCACCCCCGGGAAGCAGCGGGGTGTGGAAGC 1234  1127 TGCANCAGGAAGCTCCGGAATTANCAGGAAAACACCCACCCCCGGGAAGCGGGGTGTGCAAGCCCTICAGCACTTANCACCTTGTGCACTTGTTGTTGTTTGTTGTTTGTTGTTGTTGTTGTTGTTGT	

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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                            Virology 135 (1), 157-167 (1984)
                                                                                                                                                                                                          sarcoma virus (FSV) transforming protein p130, the product of gag-fps fused gene. p130 is highly homologous to the gag-fes sequence of feline sarcoma virus (see separate entries), and is homologous in the 280 residue carboxyl end (including the phosphoacceptor tyrosine residue) of Rous sarcoma virus p60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 4788)
Shibuya, M. and Hanafusa, H.
Nucleotide sequence of Fujinami sarcoma virus: evolutionary
relationship of its transforming gene with transforming gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACF 4788 bp ss-RNA lines
Fujinami sarcoma virus (unintegrated circular),
J02194 K01827 K01828
J02194.1 GI:209686
                                                                                                                                                                                                                                                                                                              Original source text: FSV (Fujinami sarcoma virus), unintegrated circular DNA [1],[2].
The sequence of 1182 amino acids was deduced from the Fujinami
                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1832 to 1881; 2851 to 2902)
Carlberg,K., Chamberlin,M.E. and Beemon,K.
The avian sarcoma virus PRCII lacks 1020 no transforming gene
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus
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Fujinami sarcoma virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sarcoma viruses
                   /note="5' LTR"
247. .267
                                                                         /organism="Fujinami sarcoma virus"
/mol_type="genomic RNA"
/db_xref="taxon:11885"
                                                                                                                                                                 Location/Qualifiers
  /note="5'
terminal repeat"
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    GCAAGTACCAGGAGGCCAGCAAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGC
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                                                                                                                                                   AGACCTACAGCGAGCAGTGGCAGCAGCTGCAGCAGGAGCTCACCAAGACCCCACAGCCAGG
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                                                                                TGGCAGCGGGGCCGCTGGCCAAGCTGAGCATACTGATCCGTGACAAGCAGCAGCTTCGCA
                                                                                                                                                                                                                                      TGAACTCAGGGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCA 411
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lyspeswdpitaaltonemoligesgelktwgglylgalkareeqotseqaktwgligg
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grvsppgpegiekpaterridkegetypgtbwapegrtapktygtscyhggtalgcu
catasappppyvgsglypslacyggqggdtprgaboprabpertglappalitdw
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aribeelasgapppyvwgylviktegpawtplebeklagavcagglespiavagve
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tqasesrhilhdcsaapshqdbsamgropelwcpkgftellicoselkeltsgotelsgotrk
goraksdreyagmlhhdfsqlekgeglghlrartbsgolgeswavlasgotelkgyrslv
rdstqaksdreyagmlhhdfsqlekgeglghlrartbsgolgeswavlasgotelkgyrslv
RDstqakkgdreyaghlaklgilirokolekgeglghlrartbsgolgyakthhhhycra
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lpthleslyslogewylvlkeilgeycsitslyogbvlhigkyahalmhisgifspr
gravsskorkwelgyslekgelalspeervhligkropevlaltiesgylsvlsvl
grophilpevgligeppalplogbarstolekgropevlsvlkyl
mdgqrhfiighlarklgbesppalplogbrogsakstdgrevalktikkhisgifspr
fslppvplipevgklegeppalplogbotegreagpripkresgyllsvl
wdgqrhfiighadmlyrledbgrogsrasgebgvysstggelkwkkikkeloearik
ochholivrligvcokopivgsgelraksgerlkwkkkrocarikk
vlnhebvgrasgebowsfgillwergsgelgavysalsgodyraleppegcp
mexplaysgesdywsfgillwergsgalydhalsqotrealeggorp
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1550. .4171
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/codon_start=1
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0; Mismatches 61
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Petropoulos, C.J.
Appendix 2: Retroviral taxonomy, px
genetic maps
(in) Coffin, J.M. (Ed.);
RETROVIRUSES: 757;
Cold Spring Harbor Laboratory Press
                                                                                                                                                                                  64 ACAGCACTATGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGC
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Submitted (12-NOV-1997) NIH,
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Chappey, C.
                            TCAAGAGTGACAGGGAGTATGCAGGACTGCTTCACCACATGTCC-----CTGC
                                                                             GGCTGCAGGACAGCGAGTTGCGCCTCCTGGAGCTGATGAAGAAGTGGATGTCACAGCGTG
  CTAAGAGCGACCGGGGAGTACGCGGGGATGCTGCACCACGTTCTCTCAGCTGGAGAAAC
                                                                                                      AAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGG
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USA (1997)
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llarity 66.3%;
Conservative
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LYSPGGWDPITAALTQRAMVLGKGGELKTWGLVLGALKARAERGVTSBQAKFMLGLGG
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GRVSPGGPECIEKPATERRIDKGETTVORDTVAAPEETATPKTVGTSCYHCGTALGGA
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AR IRBELASTGPPMVAMPVVIKTEGPAMTPLERKLIAGAVGAGGLESPIAVAGVE
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TQASESRHRLPHCSAAPSHQDUSAAMGFCPELWCPKGHTELLRLQDSELAKLLELMKKWM
SQRAKSDREYAGMLHHMFSQLEKQEGLGHLRATDHSSQIGESWMVLASQTETLSQTLR
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FSLPPPVFLIEBCGCELALSPCARTICKTSCGTFLKAKFUCARALL
WDGQPRHFIIGAADNLYRLEDDGLFTIFLIEDHLLGSKRPITKSGIVTLTRAVLKDKW
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BDVYRLMQRCWSCBSDVASFGILLLMEAFSLGAVFXANLSNQQTREAIEGGVRLEPPEQCP
BDVYRLMQRCWSDDPHRRPSFGAVHQDLIAIRKRHR"

JBO. 835

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4196. .444
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/protein_id="AAC82565.1"
/db_xref="GI:2801467"
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/db_xref="taxon:11885"
                                                                                                                                                                                                                                                                                                                                                                            /product="CA"
1307. .3925
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899. .1087
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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 856)
Van de Ven,W.J.M., Roebroek,A.J.M. and
Recombinant DNA and CDNA, mRNA, protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of detecting tumor cells
Patent: BP 0246709-A 2 25-NOV-1987;
Stichting Katholieke Universiteit
GGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGAACCGCACCTGAGG
                                                                                                                                                                                                                                                            CCATCTACATCGTCATGGAGCTTGTGCAGGGGGGCGACTTCCTGACCTTCCTCCGCACGG
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/product="fee/fps-related protein"
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AASGGLRQVPVCWTAPEALNYGRYSGSEDVWSFGILLWETFSLGASPYPNLSNQQTRE
FVEKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation
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/mol_type="unassigned RNA"
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                                                                                                                                                                                                                                                                                                     the transforming polyprotein of the snyder-theilen strain of feline sarcoma virus (fesv) include the transforming gene (fes) product with tyrosine specific protein kinase activity. the encoded protein sequence was compared with the gene products of gardner-armstein (ga) strain (see fesvgaonc), fps gene of avian fujinami sarcoma virus (see fev), and src gene of avian sarcoma virus the reported sequence contains a 145bp deletion against the ga strain, and the authors argue that they sequenced a defective clone, the missing nucleotides are denoted by n's (see fesvgaonc between 1818 and 1964 for presumed base sequence), the last 24 bases represent the sequence of feline leukemia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retroviruses; 1-Mammalian type C virus group.

1 (bases 1 to 2397)

1 (bases 1 to 2397)

1 (hampe, A., Laprevotte, I., Galibert, F., Fedele, L.A. and Sherr, C.J. Nucleotide sequences of feline retroviral oncogenes (v-fes) provide evidence for a family of tyrosine-specific protein kinase genes (cell 30 (3), 775-785 (1982)
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Viruses; Retroid viruses; Retroviridae; Mammalian type
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c-myc proto-oncogene;
Feline sarcoma virus
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                                                                                               GAGCAGATTGGACGGGGAACTTTGGCGAAGTGTTCAGCGGACGACGCCTGCGAGCCGACAAC
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                  ACT CTAGTGGCCGTGAAAT CTTGTCGCGAGACACTCCCACCTGACAT CAAGGCCAAGTTT
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CAGGGGCTGCAGGTAGCGCTGTGCAGCCCAGGCCAAGCTGCAGGCCCAGCAGGAGTTGCTG
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SHPNIVRLIGVCTQKQPIYIVMELVQKGDTETLETEGARLRKKTLLQWVGDAAAGME
YLESKCCIHRDLAARKCLVTEKNULKISDEGWSREEADGVYAAASGGLRLVPUKWTABA
ALNYGRYSSESDVMSFGILLMETFSLGASPYPNLSNQQTREFVEKGGRLPCPELCPDA
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382. .591
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|269. .1415
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Pred. No. 3.4e-119;
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                                                                                                                       Gardner-Arnstein feline leukemia oncovirus B Gardner-Arnstein feline leukemia oncovirus B Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses; 1-Mammalian type C virus group.

1 (bases 1 to 2946)
1 (hampe, A., Laprevotte, I., Galibert, F., Fedele, L.A. and Sherr, C.J. Nucleotide sequences of feline retroviral oncogenes (v-fes) provide evidence for a family of tyrosine-specific protein kinase genes (cell 30 (3), 775-785 (1982)
the transforming polyprotein of the gardner-arnstein strain of feline sarcoma virus (fesv) include the transforming gene (fes) product with tyrosine specific protein kinase activity. the enc protein sequence was compared with the gene products of
                                                                                                                                                                                                                                                                  c-myc proto-oncogene; fes oncogene; polyprotein.
                                                                                                                                                                                                                                                                                                 feline sarcoma virus (gardner-arnstein) transforming gene.
J02087
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                                                                                                                                                                                                                                                                                   J02087.1 GI:323872
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Local Similarity
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sarcoma virus (see fsv), and src gene of avian sarcoma virus. the
last 24 bases represent the sequence of feline leukemia virus.
Location/Qualifiers
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ACCCTGGTGGCGGTGAAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTT
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ilarity 82.8%;
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/codon_start=1
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/db_xref="GI:323873"
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/mol_type="genomic RNA"
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Pred. No. 1.6e-117;
0; Mismatches 198;
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Xenopus laevis MGC80946 protein,
IMAGE:5516233), complete cds.
Dev. Dyn. 225 (4), 384-391 (2002)
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2 (bases 1 to 4788)
                                                                   Xenopodinae: Xenopus; Xenopus.
1 (Dases 1 to 4788)
Klein,S.L., Strausberg,R.L., Wagner,L., Pontius,J.,
and Richardson,P.
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Klausner, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,
Klausner, R. D., Colline, F. S., Wagner, L., Sheamen, C. M., Schuler, G. D.,
Altechul, S. F., Zeeberg, B., Buetow, K. H., Schaefeer, C. F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,
Diatchenho, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,
Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Carrinci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,
Abramson, R. D., Mullahy, S. J., Bosak, S. A., McGwan, P. J.,
McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S.,
Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulk, S. M.,
Villalon, D. K., Muzny, D. M., Sodergen, E. J., Lu, X., Gibbs, R. A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulk, S. M.,
Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulk, S. M.,
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Worley, K. C., Hale, S., Garcia, A. M., Gardan, A., Rodrigues, S.,
Worley, K. C., Hale, S., Garcia, A. M., Gardan, A., Rodrigues, S.,
Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDMA sequences

M. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

ED Jarett Submitted (14-JUN-2004) National Institutes of Health, Xenopus Gene
Collection (XGC), National Institutes of Health, Xenopus Gene
Collection (XGC), National Institutes of Child Health, Natural Maria,
M. Berger, G. Gardan, M. M., Gardan, M. Gardan, A.
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translation="MGFAEELQCPNGHATLLRLQDTELRVMESMKKCFIQRAKGDKEY/
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2856 AGATACCGATAAGTCT 2871	2319 CGGCATCGGTGAGGCT 2334	2796 GATCCAAAGAAGCGGCCTAATTTCAGCATTGTGCATCAGGTGCTTGTCACCATCCGCAAG 2855	2259 GAGCCTGGGCAGCGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAGAGCATCCGAAAG 2318	2736 CTTGTCCCAGATAACTGCCCTGATGAAGTCTATAGCTTGATGCTGAGATGCTGGGAATAT 2795	2199 CCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAGTGCTGGGCCTAT 2258	2676 CCTTATGCAGCTATGACCAACCAGCAAACAAGGGAGGCCATAGAACAGGGAGTTCGTCTG 2735	2139 CCCTATCCCAACCTCAGCAATCAGCAGACACGGGAGTTTGTGGAGAAGGGGGGCCGTCTG 2198	2616 GAGAGTGATGTTTGGAGTTTTGGTATCTTTACTCTGGGAAGCCTTCAGCTTGGGTTCTGTT 2675	2079 GAAAGCGACGTGTGGAGCTTTGGCATCTTGGCATCTTGGGAGACCTTCAGCCTGGGGGCCTCC 2138	2556 AAGCAGATTCCTATTAAATGGACGGCGCCAGAAGCCCTCAATTACGGTCGGT	2019 AGACAAGTCCCCGTGAAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTCC 2078	2496 AGTGACTTTGGCATGTCCAGAGAAGAAGAAGATGGAGTGTATTCATCCACTGGGGGGATG 2555	1959 AGTGACTTTGGGATGTCCCGAGAGGAAGCCGATGGGGTCTATGCAGCCTCAGGGGGCCTC 2018	2436 ATTCACAGGGACCTTGCAGCCCGTAACTGTCTGGTCACTGAGAAAAATGCCTTAAAGATA 2495	1899 ATCCACCGGGACCTGGCTGGGAACTGCCTGGTGACAGAGAAGAATGTCCTGAAGATC 1958	2376 CTTATTAGGGTGTCAGAAAATGCTGCGGCTGGAATGGAGTATTTGGAGAGTAAACATTGT 2435	1839 CTGCTGCAGATGGTGGGGGATGCAGCTGCTGGCATGGAGTACCTGGAGAGAAGTGCTGC 1898	2316 CAAGGTGGAGACTTTCAGACGTTTCTACAGAATGAAGGTCCCAGGCTGAAGGTGAAAGAG 2375	1779 CAGGGGGGCGACTTCCTTCCTCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACT 1838	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0
seq length: 2000000000
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1: /cgn2=6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2=6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2=6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2=6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

5: /cgn2=6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2=6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

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9: /cgn2=6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2=6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

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15: /cgn2=6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

16: /cgn2=6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

16: /cgn2=6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

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19: /cgn2=6/ptodata/2/pubpaa/US10 PUBCOMB.pep:*

19: /cgn2=6/ptodata/2/pubpaa/US10 PUBCOMB.pep:*
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US-10-376-564-63

14 US-10-376-564-63

16 US-10-664-421-69

16 US-10-664-421-69

16 US-10-464-805-30

US-08-987-689A-30
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US-10-660-763-2
US-10-003-295-4
US-10-660-763-4
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Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 64, Appli
Sequence 64, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 69, Appl
Sequence 30, Appl
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13, Appl	12, Appl	7, Appl		•		ı, Appli	Appl	Appl	11, Appl	, App	85, Appl	), Appli	746, App	181, App		7	•	153, App					29, Appl	40, Appl	858, App	801, App	0	75, Appl	2, Appl	6, Appl

## ALIGNMENTS

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Sequence 2, Application US/10003295

| Sequence 2, Application No. US20020168741A1
| GENERAL INFORMATION:
| APPLICANT: GAN, Weiniu et al.
| APPLICANT: GAN, Weiniu et al.
| TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
| TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
| TITLE OF INVENTION: THEREOF
| FILE REFERENCE: CL001183DIV
| CURRENT FILING DATE: 2001-12-06
| UNMBER OF SEQ ID NOS: 4
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 2
| LENGTH: 752
| TYPE: PRT
| ORGANISM: Homo sapiens
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                          QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF 180
                                                                                        RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW
                                                                                                                  RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW 120
                                                                                                                                                                                MGFSSELCS PQGHGVLQQMQEAELRLLEGMRKMMAQRVKSDREYAGLLHHMSLQDSGGQS
QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF
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240

180

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RESULT 2
US-10-660-763-2
Sequence 2, Application US/10660763
Publication No. US20040063130A1
GENERAL INFORMATION:
APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001183DIVII
CURRENT APPLICATION NUMBER: US/10/660,763
CURRENT FILING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 4
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 752
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                            Query Match
Best Local S
Matches 752
                                                                                                           'Match 100.0%; Score 3879; DB 15;
Local Similarity 100.0%; Pred. No. 2.8e-223;
Les 752; Conservative 0; Mismatches 0;
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 RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW 120
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                                                       PQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS
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                                                                                                        RESULT 3
US-10-003-295-4
; Sequence 4, Application US/10003295
; Publication No. US20020168741A1
; GENERAL INFORMATION;
; APPLICANT; GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE OF INVENTION NUMBER: US/10/003,295
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTMARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 822
; Type: PRT
; ORGANISM: Homo sapiens
US-10-003-295-4
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nilarity 91.5%;
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Pred. No. 1.5e
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Sequence 4, Application US/10660763
; Sequence 4, Application US/20040063130A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PRITILE OF INVENTION: ACID MOLECULES ENCODING
TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIVII
; CURRENT APPLICATION NUMBER: US/10/660,763
; CURRENT FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-660-763-4
                    -10-660-763-4
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RESULT 5
US-09-886-319A-64
Sequence 64, Application US/09886319A
Publication No. US20020086019A1
GENERAL INFORMATION:
APPLICANT: Werner, Sabine
APPLICANT: Halle, Jorn-Peter
APPLICANT: Halle, Jorn-Peter
APPLICANT: Regenbogen, Johannes
APPLICANT: Goppelt, Andreas
TITLE OF INVENTION: Use of Polypeptides or Nucleic Aci
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TITLE OF INVENTION: Healing and for the Identification of TITLE OF INVENTION: Active Substances FILE REFERENCE: 50125/014002 CURRENT APPLICATION UNMBER: US/09/886,319A CURRENT FILING DATE: 2001-06-20; PRIOR PELLING DATE: 2000-08-01 PRIOR FILING DATE: 2000-08-01 PRIOR FILING DATE: 2000-08-01 PRIOR PELLING DATE: 2000-08-01 PRIOR APPLICATION NUMBER: DE 10030149.5 PRIOR APPLICATION NUMBER: DE 10030149.5 PRIOR FILING DATE: 2000-06-20; NUMBER OF SEQ ID NOS: 84

SOFTMARE: FeastSEQ for Windows Version 4.0; SEQ ID NO 64

LENGTH: 822
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ORGANISM: Homo sapiens
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                                                                                                ELKLKQLVKFSLDAAAGMLYLESKNCIHRDLAARNCL
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45.5%; Pred. No. 2.6e-102;
ative 150; Mismatches 217;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 822;
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Best Local Similarity 45.5
Matches 376; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wolf, Eckhard
APPLICANT: Werner, Sabine
APPLICANT: Halle, Jorn-Peter
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TYPE: PRT
ORGANISM: Homo
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                                                                                                                                                                                                                                              ELTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNBEENTHPR-ERVQLLGKRQ 358
                                                                                                                                                                                                                                                                                                                                            EVVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLN
                                                                                                                                                                                                                     NLTAESLOVMLKTLAEELMOTOOMLLNKEEAVLELEKRIEESSETCEKKSDIVLLLSOKO
                                                                                                                                                                                                                                                                                                                 EIVNVHKEIOMSVEOIDPSTEYNNFIDVHRTTAAKEQEIEFDTSLLEENENLOANEIMWN
                                                                          GRTPTLEILKSHISGIFR-PK----
                                                                                                                       ALEELKQSVQQLRCTEAKFSAQKELLEQKVQENDGKEPPPVVNYEEDARSVTSMERKE--
                           -RLSKFESIRHSIAGIIRSPKSAVGSSALSDMISISEKPLAEQDWYHGAIPRIEAQELLK
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FSNLYRLEGEGFPSIPLLIDHLLSTQ

464

438 416 418 358 299

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APPLICANT: Regenbogen, Johannes

APPLICANT: Goppelt, Andreas

ITITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for

ITITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for

ITITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound

ITITLE OF INVENTION: the Diagnosis or Treatment of Pharmacologically

ITITLE OF INVENTION: Active Substances

FILE REFERENCE: 50125/014003

CURRENT APPLICATION NUMBER: US/10/376,564

CURRENT PILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 09/886,319

PRIOR APPLICATION NUMBER: US 09/886,319

PRIOR APPLICATION NUMBER: US 06/222,081

PRIOR FILING DATE: 2001-06-20

NUMBER OF SEQ ID NOS: 86

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 64

I TANGER OF SEQ ID NOS: 86

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                             y Match 47.8%; Score 1853; DB 14;
Local Similarity 45.5%; Pred. No. 2.6e-102;
hes 376; Conservative 150; Mismatches 217;
                                                                                                                                                                                                                                                           61 RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW
                                                                                                                                                                                                                                                                                                           HMLHNOYVLALKGAQLHQNQYYDITLPLLLDSLQKMQBEMIKALKGIFDEYSQITSLVTE
                               FAHHNRYVLGVRAAQLHHQHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQD
                                                                                                                                         QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEA-SKDKDRDKAKDKYVRSLWKL
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APPLICANT: Werner, Sabine
APPLICANT: Halle, Jorn-Peter
APPLICANT: Regenbogen, Johannes
APPLICANT: Goppelt, Andreas
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
TITLE OF INVENTION: Active Substances
FILE REPERENCE: 50125/014002
CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 823
TYPE: DET
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ORGANISM: Mus musculus
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179
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||| ||:|: | || ||| ||:|: |
MGFGSDLKNSQ-EAVL-KLQDWELRLLETVKKFMALRIKSDKEYAYTLQNLCNQVDKEST
                                                                                                                                                          VQVNYVSNVSKSWLLMIQQTEQLSRIMKTHAEDLNSGPLHRLTMMIKDKQQVKKSYVGIH 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RLRVKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVY
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                                                                                                 QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEA-SKDKDRDKAKDKYVRSLWKL
                                                                                                                                                                                                 RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW 120
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                                 PAHHNRYVIGVRAAQIHHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQD 239
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                                                                            QQIEAEMIKVTKTELEKLKSSYRQLIKEMNSAKEKYKEALAKGKETEKAKERYDKATMKL
                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                         47.2%; Score 1829.5; DB 9; Length 823; 45.6%; Pred. No. 6.5e-101; ative 146; Mismatches 219; Indels 85;
                                                                                                                                                                                                                                                                                                                         85;
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US-10-376-564-63

Sequence 63, Application US/10376564

Publication No. US20030180302A1

GENERAL INFORMATION:

APPLICANT: Werner, Sabine

APPLICANT: Werner, Sabine

APPLICANT: Halle, Jorn-Peter

APPLICANT: Regenbogen, Johannes

APPLICANT: Regenbogen, Johannes

APPLICANT: Regenbogen, Johannes

TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for

TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound

TITLE OF INVENTION: Healing and for the Identification of Pharmacologically

TITLE OF INVENTION: Active Substances

FILE REFERENCE: 50125/014003

CURRENT APPLICATION NUMBER: US/10/376,564

CURRENT FILING DATE: 2003-02-28
                                                      PRIOR APPLICATION NUMBER: US 09/886,319
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: DE 100 30 149.5-41
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 86
SOPTWARE: FRAETSEQ for Windows Version 4.0
SEQ ID NO 63
LENGTH: 823
; TYPE: PRT; ORGANISM: Mus musculus US-10-376-564-63
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US-10-664-421-69
; Sequence 69, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHIMAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MANDIYAN, WICHAEL V.
APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KIN
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
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                                                                                                                                                                                                                      APPLICANT: WOMAMADI, MOOSA
APPLICANT: SCHLESSINGER, JOSEPH
APPLICANT: HUBBARD, STEVAN R.
ITILE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-
ITILE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REFERENCE: 038602/0847
CURRENT APPLICATION NUMBER: US/10/763,418
CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US/09/664,526
PRIOR APPLICATION NUMBER: US/09/664,526
PRIOR APPLICATION NUMBER: 09/09/664,526
PRIOR APPLICATION NUMBER: 09/09/664,526
PRIOR APPLICATION NUMBER: 09/01,191
PRIOR APPLICATION NUMBER: 09/701,191
PRIOR APPLICATION NUMBER: 08/701,191
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1966-08-21
NUMBER OF SEQ ID NOS: 41
SOPTWARE: PRECENTIN Ver. 2.1
SOPTWARE: 275
TYDE: DET
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PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 69
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo
US-10-664-421-69
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US-10-763-418-38
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                                                                                                Query Match
Best Local S
Matches 274
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Best Local Similarity 99.7%;
Matches 291; Conservative
                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo
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                                                                                                                    Similarity
                                            AVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDLKAKFLQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVYAASGGSRQVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVYAASGGLRQVPVKWTAPEALNYGRYSSESDVWSFGI1LWETFSLGASPYPNLSNQQTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGARLRVKTILLOMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCRETLPPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRT
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                                                                                                    Conservative
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Pred. No. 2e-83;
0; Mismatches 1;
                                                                                                  Score 1444; DB 16;
Pred. No. 1.9e-78;
0; Mismatches 1;
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                                                                   RESULT 12
US-08-987-689A-30
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              Sequence 30, Application US/08987689A Publication No. US20020048782A1 GENERAL INFORMATION:
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-10-464-805-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 038602/0116
CURRENT APPLICATION NUMBER: US/10/464,805
CURRENT FILING DATE: 2003-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LEV, SIMA
APPLICANT: SCHLESSINGER, JOSEPH
TITLE OF INVENTION: PYK2 RELATED PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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Local Similarity 67.1%;
hes 169; Conservative 3
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                                                                                                                                           NRPKFSDLHKEL
                                                                                                                                                                          QRPSFSTIYQEL 744
                                                                                                                                                                                                                           VWSFGILLWEIFSLGASPYPNLSNQQTREFVEKGGRLPCPELCPDAVFRLWEQCWAYEPG
                                                                                                                                                                                                                                                                                                    DLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPEALNYGRYSSESD 672
                                                                                                                                                                                                                                                                                                                                                                       IGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTLLQMVGDAAAGMEYLESKCCIHR 612
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                                                                                                                                                                                                               VWSFGILLWEIFSLGVCPYPGMINQQAREQVERGYRMSAPQNCPEEIFIIMMKCWDYKPE
                                                                                                                                                                                                                                                                                                                                                   IGVCTQRQPVYIIMELVPGGDFLSFLRKRKDELKLKQLVRFSLDVAAGMLYLEGKNCIHR
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Pred. No. 1.1e-46;
6; Mismatches 45;
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-987-689A-30
                                                  RESULT 13
US-10-292-524-30
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Best Local Similarity 66.7
Matches 168; Conservative
Sequence 30, Application US/10292524 Publication No. US20030119067A1 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 23/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/460,626
FILING DATE: June 2, 1995
APPLICATION NUMBER: 08/357,642
FILING DATE: December 15, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,824
FILING DATE: December 11, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
LENGTH: 251 amino acid
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APPLICATION NUMBER: US
FILING DATE: December
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: JOSEPH Schlessinger
TITLE OF INVENTION: PYKZ RELATED PRODUCTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
STREET: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows Version 2.0
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STATE: California
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                                                                                                                         NRPKFSDLHKEL
                                                                                                                                                                                           VWSFGILLWEITSLGVCPYPGMTNQQAREQVERGYRMSAPQNCPBEIFTIMMKCWDYKPE
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633 West Fifth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.2%; Score 899; DB 8; 66.7%; Pred. No. 5.8e-46; tive 36; Mismatches 46
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APPLICANT: Sima Lev

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Query Match
Best Local Similarity
Matches 168; Conserv
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/110
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: December 15, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOSEPH Schlessinger
TITLE OF INVENTION: PYK2 RELATED PRODUCTS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                     121
240 NRPKFSDLHKEL 251
                                                                                                                                                                                                                                                                                                   553 IGVCTOKOPIYIVMELVOGGDFLTFLRTEGARLRVKTLLOMVGDAAAGMEYLESKCCIHR
                                                                                                                                                                                                                                                                                                                                                                                        493 LGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDLKAKFLQEARILKQYSHPNIVRL 552
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                                                                                                                                                                     DLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPEALNYGRYSSESD
                                        QRPSFSTIYQEL 744
                                                                                                                      VWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLPCPELCPDAVFRLMEQCWAYEPG 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/292,524
FILING DATE: 13-No. US20030119067A1-2002
CLASSIFICATION: <UNKnown>
                                                                                     VWSFGILLWETFSLGVCPYPGMTNQQAREQVERGYRMSAPQNCPEEIFTIMMXCWDYKPE 239
                                                                                                                                                                                                                                                        LGELLGKGNFGEVYKGTLK-DKTPVAVKTCKEDLPQELKIKFLQEAKILKQYDHPNIVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   23.2%; Score 899; DB 14; 66.7%; Pred. No. 5.8e-46; ative 36; Mismatches 46;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-187-46
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; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/193,339
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/193,205
; PRIOR FILING DATE: 2000-03-30
; PRIOR FILING DATE: 2000-03-30
; PRIOR FILING DATE: 2000-04-05
; PRIOR FILING DATE: 2000-04-05
; PRIOR FILING DATE: 2000-04-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 17.3%; Score 669.5; DB 10; Best Local Similarity 49.4%; Pred. No. 3e-32; Matches 128; Conservative 50; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Burgess, Catherine APPLICANT: Gusev, Vladimir Y
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SOFTWARE: Patentin Ve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/195,088 FILING DATE: 2000-04-06
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239
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                                        726
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                                                                                                                         RYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLPCPBLCPDAVFRLMEQ 725
                                                                                                                                                                         KNFVHRDLAARNCLVGENKTVKIADFGLARDLYDDDYYRVKGG--KLPVRWMAPESLKYG
                                                                                                                                                                                                               KCCIHRDIAARNCIVTEKNVIKISDFGMSRE-EADGVYAASGGIRQVPVKWTAPEAINYG 665
                                                                                                                                                                                                                                                              NIVKLLGVCTEEEPLMIVMEYMEGGDLLDYLRKNRPNELSLSDLLSFALQIARGMEYLES
CWNEDPEDRPTFSELVERL 257
                                        CWAYEPGORPSFSTIYQEL 744
                                                                                                                                                                                                                                                                                                                                                LTLGKKLGEGAFGEVYKGTLKGKGGKKVEVAVKMLKEDASESQIEEFLREAKIMRKLKHP
                                                                                   KFTSKSDVWSFGVLLWEIFTLGESPYPGMSNQEVLEYLKKGYRLPQPPNCPDEIYDLMKQ
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Shimkets, Richard A
Spaderna, Steven K
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Padigaru, Muralidhar
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PRIOR APPLICATION NUMBER: 60/221,337
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-31
PRIOR PILING DATE: 2000-07-31
PRIOR PILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,135
PRIOR PILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,688
PRIOR PILING DATE: 2001-01-24
PRIOR PILING DATE: 2011-02
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; CTHER INFORMATION: Description of Artificial Sequence: Tyrosine; OTHER INFORMATION: kinase Consensus Sequence
US-09-863-776-42
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CURRENT APPLICATION NUMBER: US/09/863,776
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 09/540,763
PRIOR FILING DATE: 2000-03-30
PRIOR PILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 60/206,688
PRIOR APPLICATION NUMBER: 60/206,688
PRIOR APPLICATION NUMBER: 60/206,688
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                              Query Match 17.2%; Score 668.5; DB 10; Best Local Similarity 49.0%; Pred. No. 3.4e-32; Matches 127; Conservative 53; Mismatches 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: No. US20030198953A1el Proteins and Nucleic Acids Encoding Same
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APPLICATION NUMBER: 60/219,507
FILING DATE: 2000-07-20
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APPLICATION NUMBER: 60/209,451
FILING DATE: 2000-06-05
APPLICATION NUMBER: 60/210,060
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                                                             548 NIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGAR-LRVKTLLQMVGDAAAGMEYLES 606
                                                                                                                                                                                                                                     491 LVLGEQIGRGNFGEVFSGRLR---ADNTLVAVKSCRETLPPDLKAKFLQEARILKQYSHP 547
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Spaderna, Steven K
Shenoy, Suresh G
Rastelli, Luca
NIVKLLGVCTEEEPLMIVMEYMEGGDLLDYLRKNRPKELSLSDLLSPALQIARGMEYLES
                                                                                                                                                       LTLGKKLGEGAFGEVYKGTLKGKGGKEVEVAVKTLKEDASEQQIEEFLREAKIMRKLDHP
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Search completed: March 18, 2005, 16:12:24 Job time: 148 secs

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Result
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Listing first 45 summaries
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Maximum DB
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Perfect score:
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

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Sequence 38, Appl
Sequence 38, Appl
Sequence 62, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 6798, Ap
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Sequence 930, Appl
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GENERAL INFORMATION:

APPLICANT: GAN, Weiniu et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLICO1183DIV

CURRENT APPLICATION NUMBER: US/10/003,295

CURRENT FILING DATE: 2001-12-06

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASUSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 752

TYPE: PRT

ORGANISM: Homo sapiens

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                                                                VVAIHREMAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE
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                                                                                                                                                                    QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF
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                                               VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE
                                                                                                          AHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHBEMACILKEILQEYLEISSLVQDE
                                                                                                                           AHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE
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APPLICANT: GAM., Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001183
CURRENT APPLICATION NUMBER: US/09/817,180
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 822
TYPE: PRT
ORGANISM: Human
US-09-817-180-4
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 \VAIHREMAAAAARRIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE
                                                              AHHNRYVLGVRAAQLHHQHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE
                                                                                                       QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF
                                                                                                                        QQLQQELTKTHSQDIEKLKSQYRALLARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF 180
                                                                                                                                                                   RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW
                                                                                                                                                                                    raispdspisoswaeitsoteglsrlirohaedlnsgplsklsllireroolkktyseow
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                                               AHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                      98.8%;
                                                                                                                                                                                                                                                                                        Score 3834; DB 3;
Pred. No. 1.6e-258;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                     Length 822;
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240

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Sequence 4, Application US/10003295

| Patent No. 6686187
| Patent No. 6686187
| GENERAL INFORMATION:
| APPLICANT: GAN, Weiniu et al.
| TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
| TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND
| TITLE OF INVENTION: THEREOF
| FILE REFERENCE: CL001183DIV
| CURRENT APPLICATION NUMBER: US/10/003,295
| CURRENT FILING DATE: 2001-12-06
| NUMBER OF SEQ ID NOS: 4
| SOPTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 4
| LENGTH: 822
| TYPE: PRT
| ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                      MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKMMAQRVKSDREYAGLLHHMSLQDSGGQS
QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF 180
                                                               RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW
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                                                                                                       MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS
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                                                                                                                                                                 Conservative
                                                                                                                                                            98.8%; Score 3834; DB 4;
91.5%; Pred. No. 1.6e-258;
cive 0; Mismatches 0;
                                                                                                                                                                                             DB 4; Length
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                                                                                                  Sequence 666, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and
FILE REFERENCE: 15966-542
CURRENT FAPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
LENGTH: 822
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               FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P07332
                                                                        LENGTH: 822
TYPE: PRT
ORGANISM: Homo sapiens
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; Sequence 64, Application US/09886319A
; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or
                                                                           RESULT 6
US-09-886-319A-64
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Best Local Similarity
Matches 751; Conserv
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                                                                                                                                             QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP
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ilarity 91.4%;
Conservative
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Pred. No. 4.2e-258;
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TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound TITLE OF INVENTION: Healing and for the Identification of Pharmacologically TITLE OF INVENTION: Active Substances
FILE REFERENCE: 50125/014002
CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-06-20
INUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
ISQ ID NO 64
LENGTH: 822
TYPE: PRT
ORGANISM: Homo sapiens
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                       ETLPPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGA
                                                                       KQGDFLVRESHGKPGEYVLSVYSDGQRRHFIIQYVDNMYRFEGTGFSNIPQLIDHHYTTK
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EKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKR

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APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
ITILE OF INVENTION: Protein-Protein Complexes and
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 941
LENGTH: 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P16591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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 476
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KQGDFLVRESHGKPGEYVLSVYSDGQRRHFIIQYVDNMYRFEGTGFSNIPQLIDHHYTTK
                                                                                                                                     ALEELKOSVOOLRCTEAKFSAOKELLEOKVOENDGKEPPPVVNYEEDARSVTSMERKE--
                                                                                                                                                                                                        NITAESLQVMLKTLAEELMQTQQMLLNKEEAVLELEKRIEESSETCEKKSDIVLLLSQKQ
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                                                                                                  GRTPTLEILKSHISGIFR-PK------
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                                                                 -RLSKFESIRHSIAGIIRSPKSAVGSSALSDMISISEKPLAEQDWYHGAIPRIEAQELLK 475
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                                ----FSNLYRLEGEGFPSIPLLIDHLLSTQ 464
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APPLICANT: Werner, Sabine
APPLICANT: Halle, Jorn-Peter
APPLICANT: Regenbogen, Johannes
APPLICANT: Regenbogen, Johannes
APPLICANT: Goppelt, Andreas
ITILE OF INVENTION: Use of Polypeptides or Nucleic Acids for
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
ITILE OF INVENTION: Healing and for the Identification of Pharmacologically
ITILE OF INVENTION: Active Substances
FILE REFERENCE: 50125/014002
CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR PILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 63
LENGTH: 823
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US-09-886-319A-63
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Patent No. 6
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APPLICANT: Werne
                                                                                                                                                                                                                                                                                                                                                 / Match 47.2%; Score 1829.5; DB 4; Length Local Similarity 45.6%; Pred. No. 4.4e-119; ndels 377; Conservative 146; Mismatches 219; Indels
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                                                                                                                                                                                                        FAHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHBEMACILKEILQEYLBISSLVQD 239
                                                                                                                                                            QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEA-SKDKDRDKAKDKYVRSLWKL 179
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                                EVVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLN
                                                                     HMLHNQYVLALKGAQLHQSQYYDTTLPLLLDSVQKMQEEMIKALKGIFDDYSQITSLVTE
                                                                                                                                        QQIEAEMIKVTKTELEKLKSSYRQLIKEMNSAKEKYKEALAKGKETEKAKERYDKATMKL
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APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbard
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
TOMPUTER: TBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastESEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,191A
                           ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                           FILING DATE: August 21, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
REFERENCE/DOCKET NUMBER:
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APPLICANT: MCHAMMADI, MOOSA
APPLICANT: SCHLESSINGER, JOSEPH
APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOM
TITLE OF INVENTION: RECEPTOR TYROSINE KINASE DOM
TITLE OF INVENTION: RECEPTOR TYROSINE KINASE DOM
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REFERENCE: 038602/0847
CURRENT APPLICATION NUMBER: US/09/664,526
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/188,809
PRIOR APPLICATION NUMBER: 09/701,191
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 41
SOPTWARE: PATENTIN VET: 2.1
SOPTWARE: PATENTIN VET: 2.1
LENGTH: 275
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TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-701-191A-38
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US-09-664-526-38
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TELEX: 67-3510
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 38, Application Patent No. 6682921
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 37.2%;
Best Local Similarity 99.6%;
Matches 274; Conservative
                                                                                                                        Best Local Sim: Matches 274;
                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                  538
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                                                                                                                                        37.2%;
Similarity 99.6%;
ARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTLLQMVGDA
                                                    AVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDLKAKFLQE
                                                                       AVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDLKAKFLQE
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                                                                                                                          Conservative
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                                                                                                                      Score 1444; DB 4; Pred. No. 7.4e-93; 0; Mismatches 1;
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                                                                                                                                                         Length 275;
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RESULT 11
US-07-857-224B-62
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                                                                                                                                                    ; PAGES: 42-52
; DATE: 1988
US-07-857-2248-62
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COUNTRY: Switzerland
ZIF: (note: this is an international post code) CH
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
                                                                           Best Local Similarity 99.6 Matches 262; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 62, Application US/07857224B Patent No. 5958784
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (International TELEX: none INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 262
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APPLICANT: Benner
                                                                                                                                                                                                                                                                                                                                   ORGANISM: human FEATURE: Protein kinase; Table 8 Column PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 28
TELEFAX: (International) 41 1 262 2437
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TITLE OF INVENTION: Predicti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                    JOURNAL: SC1
VOLUME: 241
                                                                                                                                                                                                                           AUTHORS: Hunter, T.
TITLE: The protein kinase
JOURNAL: Science
                                                                                                                                                                                                                                                                                 AUTHORS: Hanks, S. K. AUTHORS: Quinn, A. M.
                                                                                                                                                                                                                                                                                                                                                                                                                      DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Zurich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Steven A. Benner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
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                                     489
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EDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDLKAKFLQEARILKQYSHPN 548
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                                                                                         35.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62:
                                                                         Score 1364.5; DB 2;
Pred. No. 2.4e-87;
0; Mismatches 0;
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                                                                           Indels
                                                                                                            Length
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                                                                           1;
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; PAGES: 42-52
; DATE: 1988
US-07-857-224B-63
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                                                                                                                                                                                                                                                                                                                                                            IELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 262
TYPE
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Patent No. 5958784
Query Match
Best Local Similarity 97.
Matches 257; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: (note: this is an international post code) CH-8092 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                   AUTHORS: Quinn, A. M.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase f.
JOURNAL: Science
VOLUME: 241
                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437
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                                                                                                                                                                                                                                       FEATURE: Protein kinase; Table 8 Column PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Zurich
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                                                                                                                                                                                                                                                                                                            DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                                                                                                                                                         AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAAS-GLRQVPVKWTAPEALNYGRYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RE: Steven A. Benner Hadlaubstrasse 151
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 34.8%; Score 1350.5; DB 2; 97.7%; Pred. No. 2.2e-86; tive 4; Mismatches 1;
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                                                                                                                                                      family
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                                 Length 262;
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   Gaps
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US-07-857-224B-64
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US-07-857-224B-64
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                                                                                                                                                                                                                                                                                             TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Benner
                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: (note: this is an international post code)
ZIP: (note: this is an international post code)
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
                                                                                                                                                      FEATURE: Protein kinase; Table 8 Column PUBLICATION INFORMATION:
                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                   LENGTH:
TYPE: a
                                                                       AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
              PAGES: 42-9
DATE: 1988
                                             JOURNAL: SC
VOLUME: 241
                                                                                                                                                                                                                                                 TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (International) 41 1 632 2830 TELEFAX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: Switzerland
                                                                                                                                                                                     ORGANISM: chicken
                                                                                                                                         AUTHORS:
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Query Match

28.8%;

Score 1116.5;

DB 2;

Length 262;

RESULT 15

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; OTHER INFORMATION: tyrkin_6 domain US-10-003-690-8
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US-10-003-690-8
                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ROTY A.J. CUITÉS
TITLE OF INVENTION: 55033, A No. 6787345el Human Eukaryotic
TITLE OF INVENTION: and Uses Therefor
FILE REFERENCE: MNI-206
CURRENT APPLICATION NUMBER: US/10/003,690
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/248,893
PRIOR APPLICATION NUMBER: 60/248,893
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 280
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 46.3
nes 133; Conservative
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234
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                           GGRLPCPE-----LCPDAVFRLMEQCWAYEPGQRPSFSTIYQEL 744
                                                                                LLPIRWMAPESLKDGKFTSKSDVWSFGVLLWEIFTLGEQPYPGBIQQFMSNEBVLEYLKK
                                                                                                                  QVPVKWTAPEALNYGRYSSESDVWSFGIILWETFSLGASPYPN-----LSNQQTREFVEK 705
                                                                                                                                                                 EYLESKNFVHRDLAARNCLVGENKVVKISDFGLSRDLYDDDKKGESKDYYRKKGGKGGKT 173
                                                                                                                                                                                    BYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSRE-----EADGVY---AASGGLR 650
                                                                                                                                                                                                                                                                     LTLGKKLGEGAFGEVYKGTLKIE---VAVK----TLKEDAKBEFLREAKIMKKLGGKHPN 53
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  GYRLPKPENDLPISSVTCPDELYDLMLQCWAEDPEDRPTFSELVERL
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29; Mismatches 23;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 207012
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 6798
LENGTH: 1148
TYPE: PRT
ORGANISM: Human
US-09-949-016-6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-016-6798, Application US/09949016; Sequence 6798, Application US/09949016; Patent NO. 6812339; GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REFERENCE: CLOO1307
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Search completed: March 18, 2005, 16:01:08
Job time : 57 secs
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                                                                                                                                                                                                                                         ESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPEALNY 664
                                                                             ACWQWNPSDRPSFAEIHQAFETM 514
                                                                                                                   QCWAYEPGQRPSFSTIYQELQSI 747
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
1169
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length: 2000000000
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Gapop 10.0 ,
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A,Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP C,Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; F;2-822/Product: protein-tyrosine kinase fes/fps #status predicted <MAT> F;460-545/Domain: SH2 homology cSH2>
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A; Molecule type: mRNA
A; Residues: 1-718, 'S', 720-822 <ALC>
A; Cross-references: GB: X52192; NID: g29890; PIDN: CAA36438.1; PID: g29891
A; Cross-references: GB: X52192; NID: g29890; PIDN: CAA36438.1; PID: g29891
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C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A24673; A60188
C;Accession: A24673; A60188
R;Rosbroek, A.J.M.; Schalken, J.A.; Verbeek, J.S.; Van den Ouweland, A.M.W.; Onnekink,
                                                                문
                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;559-821/Domain: protein kinase homology <KIN>
F;567-575/Region: protein kinase ATP-binding motif
F;267-400dified site: myristylated amino end (Gly) (in mature form) #status predicted
F;590/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GDB:119906; OMIM:190030
A;Map position: 15q26.1-15q26.1
A;Introns: 71/3; 129/3; 162/1; 223/2; 269/2; 309/2; 350/2; 412/3; 440/3; 510/3; 51/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P07332; GB:X06292; GB:M14209; GB:M14589; NID:g31348; PIDN:CAFR; A;Clalay, M.; Antolini, F.; Van de Ven, W.J.; Lanfrancone, L.; Grignani, F.; Pelicci, P. Oncogene 5, 267-275, 1990
A;Title: Characterization of human and mouse c-fes cDNA clones and identification of the A;Reference number: A60188; MUID:90191711; PMID:2179816
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A;Residues: 1-822 <ROE>
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QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF 180
                                                                                                            RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW
                                                                                                                                                                                                 MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS
                                                                       RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW
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91.5%; Pred. No. 7.8e-141;
tive 0; Mismatches 0;
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protein-tyrosine kinase (EC 2.7.1.112) fes/fps - cat
C;Species: Felis silvestris catus (domestic cat)
C;Date: 30-Sep-1989 #sequence_revision 30-Jun-1992 #text_change 23-Feb-1997
C;Accession: A27824
R;Roebroek, A.J.M.; Schalken, J.A.; Onnekink, C.; Bloemers, H.P.J.; Van de Ven, W.J.M.
J. Virol. 61, 2009-2016, 1987
A;Title: Structure of the feline c-fes/fps proto-oncogene: genesis of a retroviral onc
A;Reference number: A27824
A;Molecule type: DNA
A;Residues: 1-820 <ROE>
C;Genetics:
A;Gene: fes/fps
C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncoge:
F;458-543/Domain: SH2 homology <SH2>
F;557-819/Domain: protein kinase homology <KIN>
F;565-573/Region: protein kinase ATP-binding motif
F;588/Active site: Lys #status predicted
F;711/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predic
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No. 1.3e-132;
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protein-tyrosine kinase-related protein - mou NyAlternate names: c-fes protein CySpecies: Mus musculus (house mouse) CyDate: 02-Jul-1996 #sequence_revision 02-Jul CyAccession: I48347; JH0112 RyWilks, A.F.; Kurban, R.R. Oncogene 3, 289-294, 1988 A;Title: Isolation and structural analysis of A;Reference number: I48347; MUID:89083198; PM A;Accession: I48347; translated from GB/EMB A;Molecule type: mRNA
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                                                                                   QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP
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GB/EMBL/DDBJ

of murine c-fes PMID:3060793

clones

02-Jul-1996

#text\_change

mouse

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A;Molecule type: mRNA
A;Residues: 678-745 <WIL>
A;Experimental source: haemopoletic cell, clone FD15
A;Experimental source: haemopoletic cell, protein kinase homology; SH2 homology
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F; 458-543/Domain: SH2 homology <SH2>
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A;Cross-references: UniPROT:P16879; EMBL:X12616; NID:g50955; PIDN:CAA31138.1; R;Wilke, A.F.; Kurban, R.R.; Hovens, C.M.; Ralph, S.J.

Gene 85, 67-74, 1989
A;Title: The application of the polymerase chain reaction to cloning members of A;Reference number: JH0112; MUID:90152381; PMID:2482828
A;Accession: JH0112
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Best Local Similarity
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                                                                                  LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLR
                                                                                                                 QEATQGLQTALCSQDKLQAQQELLQSKMEQLGTGEPPAVPLLQDDRHSTSST--EREGGR
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 CPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
                        QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLTNQQTREFVEKGHRLP
                                    QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP
                                                                    LQMMGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGIYAACSGLR
                                                                                                                                        KAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTL 590
                                                                                                                                                               SGVVLFRAVPKDKWVLKHEDLVLGEQIGRGNFGEVFSGRLRADNTPVAVKSCRETLPPDL
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82.4%; Pred. No. 6e-127;
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A;Cross-references: UNIPROT:Q90778; EMBL:X02266; NID:g63203; PIDN:CAA26155.1; PID:g8710 C;Genetics: A;Gene: C-fps A;Gene: C-fps A;Gene: T-fps A;Introns: 75/3; 133/3; 166/1; 227/2; 273/2; 313/2; 354/2; 416/3; 442/3; 512/3; 553/3; C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology C;Keywords: ATP C;Keywords: ATP
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J. Mol. Biol. 181, 175-186, 1985
A;Title: Nucleotide sequence and topography of chicle, Reference number: 150618; MUID:85160839; PMID:387: A;Accession: 150618
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
A;Residues: 1-824 <HUA>
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F;561-823/Domain: protein kinase homology <KIN>
F;569-577/Region: protein kinase ATP-binding motif
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c;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
C;Accession: I50618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.9%; Score 2635; DB 2; Best Local Similarity 62.7%; Pred. No. 1.1e-94; Matches 518; Conservative 99; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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PID: 987104:

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PPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLR

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protein—tyrosine kinase (BC 2.7.1.112) fps (clone ts) - Fujinami sarcoma virus C;Species: Pujinami sarcoma virus C;Species: Pujinami sarcoma virus C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004 C;Accession: A26898 R;Chen, L.H.; Hatada, E.; Wheatley, W.; Lee, W.H. Virology 155, 106-119, 1986 A;Fitle: Single amino acid substitution, from Glu-1025 to Asp, of the fps oncogenic pr A;Fitle: Single amino acid substitution, from Glu-1025 to Asp, of the fps oncogenic pr A;Fitle: Single amino acid substitution, from Glu-1025 to Asp, of the fps oncogenic pr A;Fitle: Single amino acid substitution, from Glu-1025 to Asp, of the fps oncogenic pr A;Fitle: Single amino acid substitution, from Glu-1025 to Asp, of the fps oncogenic pr A;Fitle: C;Comment: A26898; MUID:87044080; PMID:2877522 A;Accession: A26898; MUID:87044080; PMID:2877522 A;Accessi
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EGGRTPTLEILKSHISGIFRPKFS---
                                             ROGEREAQOQUOGEVCAQAKTOAORDMEANKEAELGSEEPPPALPLOEDROSACSTDOER
                                                                       RQVLQEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPPVLLLQDDRHSTSSSEQER
                                                                                                                                         QUBETIESVQHSLTSIBEBLLASRKAVSSKEQRVWELQVELRGBBLALSPGBRVHLLGK
                                                                                                                                                                                       QLIELTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGK
                                                                                                                                                                                                                                          VQEDVLAIHQEVAHAVEMIDPATEYSSFVQCHRYDSEVPPAVTFDESLLEEAESLEPGEL
                                                                                                                                                                                                                                                                                        VQDEVVAIHREMAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGEL
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TYPVP

protein-tyrosine kinase (EC 2.7.1.112) fp

C;Species: Pujinami sarcoma virus

A;Note: host Gallus gallus (chicken)

C;Date: 27-Nov-1985 #sequence_revision 27

C;Accession: A00636

R;Shibuya, M; Hanafusa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          c;Comment: This protein is synthesized as a gag-fps polyprotein.
C;GenetLos:
A;Genet Los:
A;Genet Los:
A;Genet Los:
C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
C;Keywords: ATF; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; polyI
F;511-596/Domain: SH2 homology <SH2>
F;610-872/Domain: protein kinase homology <KIN>
F;618-626/Region: protein kinase ATP-binding motif
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A;Title: Nucleotide sequence of Fujinami Barcoma virus:
A;Reference number: A00636; MUID:83050964; PMID:6291784
A;Accession: A00636
A;Accession: A00636
A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Residues: 1-873 < CSHI>
A;Cross-references: UNIPROT:P00530
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SG--VTALKTIKNHISGIFSPRESLPBPVPLIPEVQKPLCQQAWYHGAIPRSEVQELLKY
                    SKLYALHNQYVLAVQAAALHHHHHYQRALPTHESLYSLQQEMVLVLKEILGEYCSITSL
                                                          WKLFAHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHBBMACILKEILQEYLEISSL
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Gaps

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protein-tyrosine kinase (EC 2.7.1.112) fes - feline sarcoma virus
C;Species; feline sarcoma virus
A;Note: host Felis sp. (cat)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change \
C;Caccession: A00651
R;Hampe, A.; Laprevotte, I.; Galibert, F.; Fedele, L.A.; Sherr, \
Cell 30, 775-785, 1982
A;Title: Nucleotide sequences of feline retroviral oncogenes (v-1)
A;Reference number: A00651; MUID:83050983; PMID:6183005
A;Reference type: DNA
A;Residues: 1-609 <HAM>
A;Residues: 1-609 <HAM>
A;Cross-references: UNIPROT:P00542
C;Comment: This protein is synthesized as a gag-fes polyprotein.
                                                                                           A;Gene: fee
C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
C;Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase;
F;247-332/Domain: SH2 homology <SH2>
F;346-608/Domain: protein kinase homology <KIN>
F;354-362/Region: protein kinase ATP-binding motif
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MGFSSELCSPQGHGAEQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDGGG--
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                                                  Conservative
                                                 63.9%; Score 2479; DB 1; 61.7%; Pred. No. 7.8e-89; ive 11; Mismatches 14;
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CPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
                                                                                                                      QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP 710
                                                                                                                                                                                                                        LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLR
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CPELCPDAVFRLMEQCWAYEPGQRPSFSAIYQELQSIRKRHR
                                                                                               QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP
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protein-tyrosine kinase (EC 2.7.1.112) C;Species: feline sarcoma virus A;Note: host Felis sp. (cat) C;Date: 27-Nov-1985 #sequence\_revision C;Accession: A00652 C;Accession: A00652 A; Molecule type: DNA
A; Residues: 1-477 < HAM>
A; Cross-references: UNIPROT: P00543
C; Comment: This protein is synthesized
C; Genetics:
A; Gene: fes
A; Gene: fes Cell 30, 775-785, 1982
A;Title: Nucleotide sequences of feline retroviral oncogenes (v-fes)
A;Reference number: A00651; MUID:83050963; PMID:6183005 A.; Laprevotte, I.; Galibert, F.; Fedele, L.A.; Sherr, C.J. 775-785, 1982 as 27-Nov-1985 #text\_change fes - feline sarcoma virus (strain Snyder-Theilen) S) gag-fes polyprotein 09-Jul-2004 provide evidence

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protein

kinase homology;

SH2 homology

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protein-tyrosine kinase (EC 2.7.1.112) fer - human C;Species: Homo sapiens (man) C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-C;Accession: A31943; I57573 R;Hao, Q.L.; Heisterkamp, N.; Groffen, J. Mol. Cell. Biol. 9, 1587-1593, 1989 A;Title: Isolation and sequence analysis of a novel human tyrosine A;Reference number: A31943; MUID:89261786; PMID:2725517 A;Accession: A31943.
                                                                             A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homolo C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristyla F;2-822/Product: protein-tyrosine kinase fer #status predicted <MAT> F;460-546/Domain: SH2 homology SH2>
                                                                                                                                                                A; Cross-references:
A; Map position: 5q12
C; Function:
                F;561-821/Domain: protein kinase homology <KIN>
F;569-577/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (ir
F;591/Active site: Lys #status predicted
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A; Crose-references: UNIPROT: P16591;
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F;214-476/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;214-476/Domain: protein kinase homology <KIN>;222-230/Region: protein kinase ATP-binding motif;245/Active site: Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NQQTREFVEKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
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Pred. No. 9.7e-70;
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                                               protein-tyrosine kinase (EC 2.7.1.112)
C;Species: avian sarcoma virus PRCII
A;Note: host Gallus gallus (chicken)
C;Date: 27-Nov-1985 #sequence_revision
C;Accession: A00650
R;Huang, C.C.; Hammond, C.; Bishop, J.M.
J. Virol. 50, 125-131, 1984
A;Title: Nucleotide sequence of v-fps in the PRCII strain A;Reference number: A00650; MUID:84138803; PMID:6321783 A;Accession: A00650
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Query

Match

47.8%;

Score 1853;

BB

1;

Length

A; Molecule type:

gqì

avian

sarcoma

virus

PRCII

27-Nov-1985

#text\_change

09-Jul-2004

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avian

garcoma

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Best Local Similarity Matches 376; Conserv
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SSS-GLKQIPIKWTAPEALNYGRYSSESDVWSFGILLWETFSLGVCPYPGMTNQQAREQV
                                                                                         AASGGLRQVPVKWTAPEALNYGRYSSESDWSFGILLWETFSLGASPYPULSNQQTREFV
                                                                                                                                                                              RLRVKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVY
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                                                                                                                                                                                                                                                                                                           OPLTKKSGVVLHRAVPKD-KWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCR
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                                                                                                                                            ELKLKQLVKFSLDAAAGMLYLESKNCIHRDLAARNCLVGENNVLKISDFGMSRQEDGGVY
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0; Mismatches 217;
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protein-tyrosine kinase (EC 2.7.1.112), fps/fes homolog - fruit fly (Dr N;Alternate names: kinase-related transforming protein (fps) C;Species: Drosophila melanogaster C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-C;Accession: A39670; S11628 D; Jackson, J.; Paulson, R.F.; Kornberg, T. R;Katzen, A.L.; Montarras, D:, Jackson, J.; Paulson, R.F.; Kornberg, T. Mol. Cell. Biol. 11, 226-239, 1991
A;Title: A gene related to the proto-oncogene fps/fes is expressed at d A;Reference number: A39670; MUID:91094836; PMID:1898762
A;Accession: A39670
A;Molecule type: mRNA
A;Residues: 1-803 <KA2>
A;Cross-references: UNIPROT:P18106; EMBL:X52844; NID:97971; PIDN:CAA370 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-533 <HUA>
A;Cross-references: UNIPROT: P00541
C;Comment: This protein is synthesized as a gag-
C;Genetics:
A;Gene: ips
C;Superfamily: protein-tyrosine kinase ips; prot
C;Keywords: ATP; autophosphorylation; oncogene;
               A;Gene: dfp885D
A;Cro8=-references: FlyBase:FBgn0000723
C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-or
C;Keywords: NF2 homology <SH2»
F;438-795/Domain: SH2 homology <SH2»
F;539-799/Domain: protein kinase homology <KIN»
F;547,555/Region: protein kinase ATP-binding motif
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F;278-286/Region: protein kinase ATP-binding
F;301/Active site: Lys #status predicted</pre>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVAVKSCRETLPPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHSTSSSEQEREGGRTPTLEILKSHISGIFRPKFS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RQEEDGVYASTGGMKQIPVKWTAPEALNYGRYSSESDVWSFGILLWEAFSLGAVPYANLS
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Lys #status predicted
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Pred. No. 2.6e-49;
4; Mismatches 65
                                                                                                                                                                EMBL: X52844; NID: g7971; PIDN: CAA37036.1; PID: g7972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <KIN>
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ene; phosphoprotein; phosphotransferase;
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                                                                                                                                                                                                                                                                                             Kornberg,
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                                                                      proto-oncogene
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Query Match 29.9%; Score 1160; DB 1; Best Local Similarity 34.4%; Pred. No. 5.7e-38; Matches 284; Conservative 136; Mismatches 297;
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                                                               RETLPPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEG
                                                                                                                                                                                                                                                                      NEVGCEELPSGCDDDLTLEQNFIENGYNNEQQISLSTNRPLYEEEWFHGVLPREEVVRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSI
                                                                                                                                   NGLTTREQMGMCRDAAAGMRYLESKNCIHRDLAARNCLVDLEHSVKISDFGMSREEEE--
                                                                                                                                                               ARLRVKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSRPTSTRRFQKRIDTVIGSINPTEEYGEFTEKYKTSPTTPLLFQFDETLIQD----IPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQE-----ASKDKDRDKAKDKYVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS
                                                                                                                                                                                                      RMTLPDEQKRKFLQEGRILKQYDHPNIVKLIGICVQKQPIMIVMELVLGGSLLTYLRKNS
                                                                                                                                                                                                                                                                                                                                                                         -----REGGRIPTLEILKS-----HISGIFRPKFSNLYRLEGEGFPSIPLLIDHLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                           EHLGPGEPP----PVLLLQDDRHSTSSSEQE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLQSSTLTV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLVQDEVVAIHREMAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKIAARLNHLTDEVVRK-KSEYQKHLEGYKALRTRFEENYIKAPSRSGRKLDDVRDKYQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADEMOGSLISKSWRSYMDELDHOAKOFKFNAEQLEV-VCDKLTHLSODKRKARKAYOEEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGFSSALQSRAAHBALIVRQDAELRLMETMKRSIQMKAKCDKEYAISLTAVAQQGLKTDR
IDTGYRMPTPKSTPEEMYRLMLQCWAADAESRPHFDEIYNVVDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.9%; Score 1160; DB 1; 34.4%; Pred. No. 5.7e-38;
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rat (fragment)

#text\_change

09-Jul-2004

protein-tyrosine kinase (EC 2.7.1.112) flk - rat (fragme C;Species: Rattus norvegicus (Norway rat) C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text C;Accession: S04328 R;Letwin, K.; Yee, S.P.; Pawson, T. Oncogene 3, 621-627, 1988 R;Title: Novel protein-tyrosine kinase cDNAs related to A;Reference number: S04327; MUID:94167102; PMID:2485255 A;Accession: S04328 fps/fes and eph cloned using

anti

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A;Gene: flk
C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; tyrosin
F;62-322/Domain: protein kinase homology <KIN>
F;70-78/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-323 <LET>
A;Cross-references: UNIPROT:P09760; EMBL:X13412; NID:g56169; PIDN:CAA31778.1;
C;Genetics:
ۇ.
                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-453 <RES>
A;Cross-references: UNIPROT:Q61561; GB:M32054; NID:g193276; PIDN:AAA37617.1; PID:g30923:
C;Superfamily: protein kinase homology; SH2 homology
C;Keywords: ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Fischman, K.; Edman, J.C.; Shackleford, G.M.; Turner, J.A.; Rutter, W.J.; Mol. Cell. Biol. 10, 146-153, 1990
A;Title: A murine fer testis-specific transcript (ferT) encodes a truncated A;Reference number: I49663; MUID:90097822; PMID:2294399
A;Accession: I49663
                                                                        ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine kinase (ferT) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C;Accession: I49663
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                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                      ;91-177/Domain: SH2 homology <SH2>;192-452/Domain: protein kinase homology <KIN>;200-208/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 206;
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Best Local Similarity
                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLYRLEGEGFPSIPLLIDHLLSTQQPLTKKSGVVLHRAVPKD-KWVLNHEDLVLGEQIGR 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QPIYIVMELVQGGDFLTFLRTEGARLRVKTLLQMVGDAAAGMEYLESKCCIHRDLAARNC
                                                                              RHSTSSSEQE----PKFSNLYRLEGE 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVTEKNVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPEALNYGRYSSESDVWSFGIL 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IYQELQSIRKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LWETFSLGASPYPNLSNOQTREFVEKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPVYIIMELVPGGDFLSFLRKRKDELKLKQLVRFSLDVAAGMLYLEGKNCIHRDLAARNC
    GFPSIPLLIDHLLSTQQPLTKKSGVVLHRAVPKD-KWVLNHEDLVLGEQIGRGNFGEVFS
                                        WYHGAIPRIEAQELLKQQGDFLVRESHGKPGEYVLSVYSDGQRRHFIIQFVDNLYRFEGT
                                                                                                                     KERKERLSKFESIRHSIAGI-----IKSPKSVLGSSTVCDVISVGERP---LAEHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVGENNTLKISDFGMSRQEDGGVYSSS-GLKQIPIKWTAPEALNYGRYSSESDVWSFGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                  28.3%; Score 1097; DB 2; 53.3%; Pred. No. 8.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.3%; Score 1099.5;
66.2%; Pred. No. 4.96
tive 45; Mismatches
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                                                                                                                                                                                                  63;
                                                                                                                                                                                              Pred. No. 8.6e.
3; Mismatches
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.9e-36;
les 57;
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proto-fps protein - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_char
C;Accession: I50406
R;Pfaff, S.L.; Zhou, R.
Virology 146, 307-314, 1985
A;Title: Defining the borders of the chicken proto-fps gene,
A;Title: Defining the borders of the chicken proto-fps gene,
A;Reference number: I50405; MUID:86020620; PMID:2996222
A;Accession: I50406
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
gag-abl-pol polyprotein - feline sarcoma virus (strain N;Contains: protein-tyrosine kinase (EC 2.7.1.112) C;Species: feline sarcoma virus C;Date: 31-Dec-1988 #sequence_revision 09-Sep-1994 #tex C;Accession: A26132
                                                                                       RESULT
A26132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: |
C; Keywords: ATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q90943; GB:M11611; NID:g212542; PIDN:AAA49008.1; PID:g212545
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Best Local Sim
Matches 133;
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                                                                                                                                                                                                                                                                 PNLSNOQTREFVEKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRH 751
                                                                                                                                                                                                                                                                                                                        FGMSREEADGVYAASGGLRQVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPY
                                                                                                                                                                                                                                                                                                                                                                                               GDFLTFLRTEGARLRVKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRLRADNTLVAVKSCRETLPPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVME
                                                                                                                                                                                                                                                                                                       FGMSRQEEDGVYASTGGMKQIPVKWTAPEALNYGRYSSESDVWSFGILLWEAFSLGAVPY
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Sarc

09-Sep-1994 #text\_change

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A/Gene: gag-abl-pol
C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo C/Keywords: ATP; oncogene; phosphotransferase; polyprotein; transforming protein; tyrosi F/59-117/Domain: SH3 homology <SH3>
F/128-218/Domain: SH2 homology <SH2>
F/241-501/Domain: protein kinase homology <KIN>
F/241-501/Domain: protein kinase ATP-binding motif
F/272/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Bergold, P.J.; Blumenthal, J.A.; D'Andrea, E.; Snyder, H.W.; Lederman, L.; Silverstone J. Virol. 61, 1193-1202, 1987
A;Title: Nucleic acid sequence and oncogenic properties of the HZ2 feline sarcoma virus A;Reference number: A26132; MUID:87141338; EMID:3029415
A;Accession: A26132;
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A;Residues: 1-697 <BER>
A;Cross-references: GB:M15805; NID:g323883; PIDN:AAA43042.1; PID:g323884
C;Genetics:
Search completed: March 18, 2005, 16:00:10 Job time : 50 secs
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                                                                                                                                                    GILLWETFSLGASPYPNLSNQQTREFVEKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPS 736
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# ALIGNMENTS

RESULT 1
ABB07354
ID ABB07354
AC ABB0
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XX Homc
XX Homc US6340584-B1. Homo sapiens. gene therapy; anti-kinase. 09-APR-2002 27-MAR-2001; 2001US-00817180. 27-MAR-2001; 2001US-00817180. Proto-oncogene tyrosine kinase; poTK; tumour; cytostatic; anti-leukemic; gene therapy; protein therapy; vaccine; enzymatic-inhibition; human; Human proto-oncogene tyrosine kinase ABB07354; ABB07354 standard; (PEKE) 22-JAN-2002 PE CORP NY. Ye J, (first entry) Di Francesco V, protein; 752 Beasley EM; A

Nucleic acids encoding a proto-oncogene tyrosine kinase, prevention, diagnosis and treatment of e.g. leukemia and useful for the lung tumors.

WPI; 2002-138497/18. N-PSDB; ABA94500, ABA94501.

Claim 1; Fig 2A; 49pp; English.

The invention provides isolated nucleic acid sequences encoding a protooncogene tyrosine kinase (poTK). The poTK poJYnucleotides and protein may
be used in the prevention, diagnosis and treatment of diseases associated
with inappropriate poTK expression, such as lung and kidney tumours,
leukemia and stomach adenocarcinoma. poTK may be used to treat disorders
associated with decreased expression by rectifying mutations or deletions
in a patient's genome that affect the activity of poTK by expressing
inactive proteins or to supplement the patients own production of poTK.
The encoded poTK may be used as an antigen in the production of
antibodies against poTK and in assays to identify modulators of poTK
expression and activity. The anti-poTK antibodies and antagonists may be
used to down regulate expression and activity and as diagnostic agents

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RESULT 2
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                             Human kinase
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                            amino acid sequence.
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Pred. No. 6e-280;
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RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW

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MGFSSELCSPQGHGVLQQMQBABLRLLEGMRKMMAQRVKSDREYAGLLHHMSLQDSGGQS

MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS

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Query Match Best Local Simi Matches 752;

Similarity

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Score 3879; Pred. No. 6e Mismatches

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The invention relates to a newly isolated peptide sequence of a human CC kinase that is related to the proto-oncogene tyrosine kinase subfamily. CC The activity of the kinase of the invention may be described as, CC cytostatic, antiarteriosclerotic, antiinflammatory and antipsoriatic. CP peptides of the invention are useful in assays to determine the CC biological activity of the protein, in drug screening assays, tissue CC typing and pharmacogenomic analysis. They are also useful in treating or CC diagnosing disorders characterised by an absence of, inappropriate, or CC unwanted expression of the protein, such as inflammation, cancer (e.g. CC leukaemia, lung tumours, kidney tumours or stomach adenocarcinoma), CC arteriosclerosis, and psoriasis Nucleic acid molecules of the invention CC are useful as probes, primers and chemical intermediates in biological CC assays. The peptide and nucleic acid sequences are useful as models for the development of human therapeutic targets, aid in the identification of the development of human therapeutic targets, aid in the identification CC therapeutic proteins and serve as targets for the development of human therapeutic protein activity in cells and CC tissues that express the protein. The protein activity in cells and CC tissues that express the protein. The protein of the invention may also be useful in gene therapy. The gene encoding the protein of the invention cCC represents the human chromosome 15. The current sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human kinase protein, useful for treating or diagnosing disorders associated with an absence of, inappropriate, or unwanted expression the protein, e.g. inflammation or cancer, in drug screening assays and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1 (a); Fig 2; 75pp;
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06-DEC-2001; 2001US-00003295.
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                                                     WPI; 2004-282461/26.
N-PSDB; ADM28580, ADM28582
                              New human kinase peptides, useful for preparing a composition treating a disease or condition mediated by human kinases.
                                                                                                           27-MAR-2001; 2001US-00817180
06-DEC-2001; 2001US-00003295.
                                                                                                                                                                                                 gene therapy;
                                                                                                                                                                                                                  Human proto-oncogene tyrosine kinase
                                                                                                                                                                                                                                                                 ADM28581 standard;
 The invention relates
                Claim 1;
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                                                                                                                                                    01-APR-2004.
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                                       standard;
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Query Match 100.0%; Score 3879; DB 8; Best Local Similarity 100.0%; Pred. No. 6e-280; Matches 752; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
                                                                                                                                                                                              MEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPE
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                                                                                                             ALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEXGGRLPCPELCPDAVF
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                                                                                                                                                                          MEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPE
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feline sarcoma

virus

FES

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The invention provides isolated nucleic acid sequences encoding a proto-
concogene tyrosine kinase (poTK). The poTK polynuclectides and protein may
be used in the prevention, diagnosis and treatment of diseases associated
with inappropriate poTK expression, such as lung and kidney tumours,
leukenia and stomach adenocarcinoma. poTK may be used to treat disorders
associated with decreased expression by rectifying mutations or deletions
in a patient s genome that affect the activity of poTK by expressing
inactive proteins or to supplement the patients own production of poTK.
The encoded poTK may be used as an antigen in the production of
antibodies against poTK and in assays to identify modulators of poTK
expression and activity. The anti-poTK antibodies and antagonists may be
used to down regulate expression and activity and as diagnostic agents
for detecting the presence of poTK in samples. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 752; Conser
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                                 LTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGKRQVL
                                                                                                                               VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE
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RESULT 5
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Human kinase related amino acid sequence.

24-JAN-2003

(first entry)

Human; kinase; proto-oncogene tyrosine kinase; antiarteriosclerotic; cytostatic; antiinflammatory; antipsoriatic; gene therapy; protein kinase; drug screening assay; tissue typing; chromosome 15; pharmacogenomic analysis; inflammation; cancer; leukaemia; lung tumo stomach adenocarcinoma; arteriosclerosis; psoriasis. tumours,

Homo sapiens.

S

03-OCT-2002.

WO200277191-A2

27-MAR-2002; 2002WO-US009325

27-MAR-2001; 06-DEC-2001; 2001US-00817180 2001US-00003295

(PEKE ) PE CORP NY.

ξ Υe J, Di Francesco < Beasley 照,

WPI; 2003-029927/02

New human kinase protein, useful for treating or diagnosing disorders associated with an absence of, inappropriate, or unwanted expression of the protein, e.g. inflammation or cancer, in drug screening assays and pharmacogenomics. xpression of assays and

Disclosure; Page 74-75; 75pp; English र् 밁 S 문 8 8 S 밁 ð 밁

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CC The invention relates to a newly isolated peptide sequence of a human CC kinase that is related to the proto-oncogene tyrosine kinase subfamily. CC The activity of the kinase of the invention may be described as, CC cytostatic, antiarteriosclerotic, antiinflammatory and antipsoriatic. CC Peptides of the invention are useful in assays to determine the CC biological activity of the protein, in drug screening assays, tissue CC typing and pharmacogenomic analysis. They are also useful in treating or CC unwanted expression of the protein, such as inflammation, cancer (e.g. CC leukaemia, lung tumours, kidney tumours or stomach adenocarcinoma). CC arteriosclerosis, and psoriasis. Nucleic acid molecules of the invention CC assays. The peptide and nucleic acid sequences are useful as models for the development of human therapeutic targets, aid in the identification CC the development of human therapeutic targets, aid in the identification CC therapeutic proteins and serve as targets for the development of human therapeutic targets for the development of human therapeutic targets for the development of human cc assays. The peptide and sequence gene encoding the protein of the invention may also be useful in gene therapy. The gene encoding the protein of the invention CC has been localised to human chromosome 15. The current sequence cof the invention. NOTE: This sequence is not further mentioned in the
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                             KAKFLQEARILKQYSHPNIVRLIGVCTQKQPIXIVMBLVQGGDFLTFLRTEGARLRVKTL
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llarity 91.5%;
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Pred. No. 1.5e-276;
0; Mismatches 0;
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Matches 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a new isolated human proto-oncogene tyrosine kinase peptide or its allelic variant, orthologue or fragment. The peptide is useful for preparing a composition for treating a disease or condition mediated by a human kinase protein e.g. cancer. The present sequence represents the amino acid sequence of the human V-FES/FPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human kinase peptides, useful for preparing a composition treating a disease or condition mediated by human kinases.
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06-DEC-2001; 2001US-00003295.
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V-FES/FPS.
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                                                                                                                                                                                                                                                                         Score 3834; DB 8;
Pred. No. 1.5e-276;
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                                                                                                                                                                      Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemi
                                            18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
                                                                                                                                                                                                                   Novel human
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                                                                              16-APR-2001; 2001WO-US008656
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                       (HYSE-) HYSEQ INC
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  Liu C,
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WPI;
                                                                          Claim 20;
                                                                                 vaccination,
                                                                                             2001-611725/70
                                                                                 acids encoding a
                                                                          Page 645-646; 765pp; English.
                                                                                range of human polypeptides, useful in genetic therapy.
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The invention relates to novel human secreted polypeptides. The CC polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated CC with altered levels of polypeptide. The polypeptides are also useful for cidentifying agents (agonists and antagonists) that bind to them. Cells corpressing the proteins are useful for identifying a therapeutic agent CC for use in treatment of a pathology related to aberrant expression or CC physiological interactions of the polypeptide. Vectors comprising the cucleic acids encoding the polypeptides and cells genetically engineered CC to express them are also useful for producing the proteins. The proteins CC are useful in genetic vaccination, testing and therapy, and can be used CC as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon CC and/or nerve tissue growth or regeneration; immune suppression and/or CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias. CC AAU29510-AAU3304 represent the amino acid sequences of novel human createred contents of the invention contents of the secreted proteins of the invention.

Sequence 2202 AA;

Similarity

97.5%;

Length

2202

g S Ś 밁 밁 S 밁 ð 밁 S 밁 S 밁 Ś S 밁 Ś 당 S S Query Match Best Local S Matches 751 500 541 453 481 441 421 421 361 361 301 301 241 241 181 181 121 121 . 61 61 751; 1 MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS QEALQGIQVALCSQAKLQAQQELLQTKLEHLGPGEPPPVLLLQDDRHSTSSSEQEREGGR 420 QOLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF RAISPDSPISQSWAEITIQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW LVRESQGKQEYVLSVLWDGLPRHFIIQSLDGSRPLRMEAADPGSPALQNLYRLEGEGFPS LTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGKRQVL VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE AHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS IPLLIDHLLSTQQPLTKKSGVVLHRAVPKDKWVLNHEDLVLGEQIGR--------------TPTLEILKSHISGIFRPKFS------LTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGKRQVL AHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDB I PLL I DHLLSTQQPLTKKSGVVLHRAVPKDKWVLNHEDLVLGEQIGRVPQRGSNSQRAWV TPTLEILKSHISGIFRPKFSLPPPLQLIPEVQKPLHEQLWYHGAIPRAEVAELLVHSGDF Conservative <u>.</u> Score 3783.5; DB 4; Pred. No. 3.4e-272; 0; Mismatches 1; GNFGEVFSGRLRADNTLVAVKS Indels -----NLYRLEGEGFPS Gaps 120 120 452 480 180 180 60 60 600 499 540 440 360 360 300 300 240 240 Ν

Gaps

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                                                                                                                                                          New human kinases and phosphatases (KPP) for diagnosing, treating preventing diseases or conditions associated with aberrant KPP expectage. cancer, acquired immunodeficiency syndrome, epilepsy, or infi
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19-MAR-2003; 2003US-0456932P
28-MAR-2003; 2003US-0458844P
09-APR-2003; 2003US-0461678P
17-APR-2003; 2003US-0463937P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; kinase and phosphatase protein; KPP; enzyme; cytostatic; antiarteriosclerotic; anticrovalsant; nootropic; neuroprotective; cerebroprotective; anti-HV; antiallergic; antinflammatory; thyromimetic; gene therapy; cell proliferative disorder; cancer; thyromimetic; gene therapy; cell proliferative disorder; cancer; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; inflammatory disorder; AIDS; allergy; developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
  nootropic, neuroprotective, cerebroprotective antiinflammatory and thyromimetic activities,
                   The present sequence represents the human kinase and phosphatase posteron, designated KPP-43. The human KPP sequences from the present invention have cytostatic, antiarteriosclerotic, anticonvulsant, nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallery
                                                                                                                          Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKMMAQRVKSDREYAGLLHHMSLQDSGGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         764
                                                                                QVÞVKWTAÞBALNYGRYSSESDVWSFGILLWETFSLGAS ÞYÞNLSNQQTREFVEKGGRLÞ
                                                                                                                                                                   LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLR
                                                                                                                                                                                                                                                 KAKFLQEARILKQYSHDNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTL
                                                                                                                                                                                                                                                                                                                                                                                             LVRESQGKQEYVLSVLWDGLPRHFIIQSLDNLYRLEGEGFPSIPLLIDHPLSTQQPLTKK
                                                                                                                                                                                                                                                                                                                                                                                                                          -----NLYRLEGEGFPSIPLLIDHLLSTQQPLTKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPTLEILKSHISGIFRPKFSLPPPLQLIPEVQKPLHEQLWYHGAIPRAEVAELLVHSGDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEALQGLQVALCSQARLQAQQELLQTKLEHLGPGEPPPVLLLQDDRHSTSSSEQEREGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPPVLLLQDDRHSTSSSEQEREGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDIPPCVTFDESLLEEGEPLEPGELQLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AHHNRYVLGVRAAQLHHQHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAISPDSPISQ-----
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                                                               QVPVKWTAPEALN
                                                                                                                                             LOMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLR
                                                                                                                                                                                                                              KAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTL
                                                                                                                                                                                                                                                                                                              SGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----THSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF
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84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 3493; DB;
; Pred. No. 3.5e-2;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8;
                                                             LGASPYPNLSNQQTREFVEKGGRLP
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AC ADH4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 677; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for inducing neutralisation of cells or tissues by using a protein binding to CRAM (collapsing response mediator protein-associated molecule) protein or its encoded gene. The proteins and their encoded genes are useful in gene therapy and regenerative medicine, e.g. by inducing neutralisation of mitochondria. They are also applicable in diagnosis, drug development for neural diseases and studying the mechanism of pathosis. The current sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes and proteins participating in neutralization of cells or tissues, useful in gene therapy and regeneration medicine, applicable in diagnosis, drug development for neural diseases and study of mechanism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuroprotective; neutralisation; CRAM; collapsing-response mediator protein-associated molecule; gene therapy; mitochondria; drug development; neural disease; pathosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADH43090 standard; protein; 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004001038-A1
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DB; ADH43089.
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                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                        61 WSSGPDSPVSQSWAEITSQTENLSRVLRQHAEDLNSGPLSKLSVLIRERHSLRKTYNEQW
                                                                                                                                                                                                                 QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF
                                                                                                                                                                                                                                                                                                                                    RAISPDSPISQSWABITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW
   VVÄIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE
                                                                                             AHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE
                                                                                                                                                                                  QQLQQELTKTHSQDIEKLKTQYRTLVRDSTQARRKYQEASKDKDRDKAKDKYVRSLWKLF
                                                                                                                                                                                                                                                                                                                                                                                                                               MGFSSELCSPQGHGAVQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS
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                                                              AHHNRYVLGVRAAQLHHHHHHRFMLPGLLQSLQDLHEEMAGILKDILQEYLEISSLVQDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.5%; Scilarity 82.4%; Pr
Conservative 35;
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Pred. No. 1.2e:
35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , DB 8;
L.2e-249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemi
Nucleic acids encoding a range of vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2001
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                                                                                             WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                    16-APR-2001; 2001WO-US008656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human secreted protein
                                                                                                                                                                                                                                                                            18-APR-2000; 2000US-00552929
26-JAN-2001; 2001US-00770160
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                                  human polypeptides, useful
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Claim
20,
Page
645;
765pp; English.
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CC polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated CC with altered levels of polypeptide. The polypeptides are useful for CC identifying agents (agonists and antagonists) that bind to them. Cells CC expressing the proteins are useful for identifying a therapeutic agent CC for use in treatment of a pathology related to aberrant expression or CC physiological interactions of the polypeptide. Vectors comprising the CC useful acids encoding the polypeptides and cells genetically engineered CC to express them are also useful for producing the proteins. The proteins CC are useful in genetic vaccination, testing and therapy, and can be used CC as nutritional supplements. They may be used to increase stem cell CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon CC and/or nerve tissue growth or regeneration; immune suppression and/or CC stimulation, as anti-inflammatory agents; and in treatment of leukaemias. CC AAU29510-AAU3304 represent the amino acid sequences of novel human CC secreted proteins of the invention ő novel human secreted polypeptides: The

### Sequence 2017 **₽**

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                                                                                                                                             VFSGRLRADNTLVAVKSCRETLPPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYI
                                                                                                                                                                                                                     SPALQNLYRLEGEGFPSIPLLIDHLLSTQQPLTKKSGVVLHRAVPKDKWVLNHEDLVLGE
                                                                                                                                                                                                                                                                                                                      LLEEGEPLEPGELQLNELTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEE
                                              NVLKISDFGMSREEADGYYAASGGLRQVPVKWTAPEALNYGRYSSESDVWSFGILLWETF
                                                                                                     VMELVQGGDFLTFLRTEGARLRVKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEK
                                                                                                                                                                            QTGRVPQRGSNSQRAWVRGPNTGAPHPGVGSRMGRKRRELRDWEGRGRSPRPFQGNFGE
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     SLGASPYPNLSNOOTREFY
                         SLGASPYPNLSNOQTREFVEKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQEL
                                                                                        VMELVQGGDFLTFLRTEGARLRVKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEK
                                                                                                                                   VFSGRLRADNTLVAVKSCRETLPPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYI
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73.1%;
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Pred. No. 1.6e-169;
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20-MAY-2004
                            ADK71829;
                                                       ADK71829
                                                      standard; protein; 472 AA
(first entry)
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Human kinase and phosphatase KPP-6 protein.

antiallergic; antiasthmatic; immunosuppressive; antithyroid; dermatological; antidiabetic; nephrotropic; antigout; gastrointestinal; neuroprotective; osteopathic; antiarthritic; uropathic; ophthalmological; antirheumatic; antiparisonian; nootropic; antiparist; haemostatic; cytostatic; antilpaemic; antiparasitic; antiparasitic; antihalmintic; antibacterial; virucide; protozoacide; fungicide; cardiovascular disease; immune system; neurological; growth; development; cell proliferation; viral; bacterial; fungal; parasitic; protozoan; helminthic infection; transgenic; gene therapy; enzyme; single nucleotide polymorphism; SNP. human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic; hypotensive; vasotropic; antiinflammatory; antianginal; anti-HIV;

WO2004018641-A2

04-MAR-2004.

25-AUG-2003; 2003WO-US026635.

26-AUG-2002; 2002US-0406172P. 25-SEP-2002; 2002US-0413910P. 27-SEP-2002; 2002US-0414296P. 11-OCT-2002; 2002US-0417821P.

(INCY-) INCYTE CORP

Chang H Chawla ynn MR, Richardson Tha SD, Emerling BM, 1g H, Yang YG, Lee S la NK, Ramkumar J, 1g e J; TW. Marquis JP. Swarnakar A. Tang YT; Jin P. Wilson AD. Yue H. Gietzen KJ; e SY, Khare R. Elliott VS, Hafalia AJA; Gururajan R. Tribouley CM, Chien D, Tran

N-PSDB; 2004-226830/21. DB; ADK71888.

New human kinases and phosphatases, useful for diagnosing, treating preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, car cancer

Claim 1; ID NO 6 347pp; English

ARESULT 11
ARESULT 11
ARESULT 20
ADK71829
ADK ADK77
AC AD The invention relates to a novel isolated polypeptide which is a human CC kinase and phosphatase (KPP). The polypeptide of the invention CC demonstrates cardiovascular, antiatreriosclerotic, hypotensive, CC vasotropic, antialflammatory, antianginal, anti-HIV, antiallergic, CC antiasthmatic, immunosuppressive, antithyroid, dermatological, accompathic, antiarthritic, unopathic, ophthalmological, neuroprotective, CC antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antipsoriatic, CC antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antipsoriatic, CC antiparkinsonian, nootropic, antilpaemic, antiparasitic, antiphacterial, virucide, protozoacide and fungicide activities. The CC antiparker of the polynucleotides, polypeptides, agonists and considers and phosphatase (KPP) polynucleotides, polypeptides, agonists and CC disorders such as cardiovascular diseases, immune system disorders, cell proliferative disorders and viral, bacterial, fungal, parasitic, cell protozoan or helminthic infections. Furthermore, the molecules of the

745

QSIRKRHR 752

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ADL71055
ID ADL71
XX ADL71
XX ADL71
XX ADL71
XX OBTEC
XW OBTEC
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Matches 411; Conserv
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                                                                                                                                                                                      16-APR-2002; 2002JP-00113908
19-APR-2002; 2002US-0373594P
                                                                                                                                                                                                                                                                                                                                                                                          Osteopathic; antiinflammatory; antirheumatic; antiarthritic; gene therapy; type II collagen; expression; cartilage disease; osteoarthritis; cartilage defect; rheumatoid arthritis; human.
                                                         N-PSDB;
                                                                                                                                                                                                                                            16-APR-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Type II collagen expression
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                                                                                                                                                   (ASAH )
purified protein that promotes type preventing and treating a cartilage
                                                       2003-845331/78.
DB; ADL71054.
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Pred. No. 8.8e-147;
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II collagen expression, usefu disease, e.g. osteoarthritis,
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PT cartilage defect, or rheumatoid arthritis.

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PS Claim 1; SEQ ID NO 48; 271pp; English.

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The invention relates to a purified protein (I) that promotes type II collagen expression. Also disclosed is an isolated polynucleotide encoding (I), a recombinant vector comprising the polynucleotide and a gene therapeutic agent comprising the recombinant vector as an active ingredient. The proteins, genes, agents and methods are useful for preventing and treating a cartilage disease, e.g. osteoarthritis, cartilage defect, or rheumatoid arthritis. The current sequence represents a human protein that promotes type II collagen expression.

Sequence 822 AA;

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Query Match
Best Local Similarity 45.5
Matches 376; Conservative
715
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                 AASGGLRQVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFV
                                                                     VLQEALQGLQVALCSQAKLQAQQBLLQTKLEHLGPGEPPPVLLLQDDRHSTSSSEQEREG
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                                                      ELKLKQLVKFSLDAAAGMLYLESKNCIHRDLAARNCLVGENNVLKISDFGMSRQEDGGVY
                                                                                                           EDLPQELKIKFLQEAKILKQYDHPNIVKLIGVCTQRQPVYIIMELVSGGDFLTFLRRKKD
                                                                                                                           ETLPPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGA
                                                                                                                                                                                                                       KQGDFLVRESHGKPGEYVLSVYSDGQRRHFIIQYVDNMYRFEGTGFSNIPQLIDHHYTTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HMLHNQYVLALKGAQLHQNQYYDITLPLLLDSLQKMQEEMIKALKGIFDEYSQITSLVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQD
                                                                                                                                                                                                                                                                              -RLSKFESIRHSIAGIIRSPKSAVGSSALSDMISISEKPLAEQDWYHGAIPRIEAQELLK
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45.5%; Pred. No. 6.1e-129;
tive 150; Mismatches 217;
                                                                                                                                                                                                                                                   -----FSNLYRLEGEGFPSIPLLIDHLLSTQ
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EKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKR

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 47.1%; Score 1826.5; DB 7; Best Local Similarity 45.5%; Pred. No. 5.8e-127; Matches 376; Conservative 147; Mismatches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a purified protein (I) that promotes type II collagen expression. Also disclosed is an isolated polynucleotide encoding (I), a recombinant vector comprising the polynucleotide and a gene therapeutic agent comprising the recombinant vector as an active ingredient. The proteins, genes, agents and methods are useful for preventing and treating a cartilage disease, e.g. osteoarthritis, cartilage defect, or rheumatoid arthritis. The current sequence represents a human protein that promotes type II collagen expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 823 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 46; 271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New purified protein that promotes type II collagen expression, useful for preventing and treating a cartilage disease, e.g. osteoarthritis, cartilage defect, or rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-2002; 2002JP-00113908.
19-APR-2002; 2002US-0373594P.
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                                            HMLHNQYVLALKGAQLHQSQYYDTTLPLLLDSVQKMQEEMIKALKGIFDDYSQITSLVTE
                                                                                                                                                          QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEA-SKDKDRDKAKDKYVRSLWKL 179
                                                                                                                                                                                                                                                                     RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW 120
                                                                                                                                                                                                                                                                                                                                                MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS
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  EVVAIHREMAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLN 299
                                                                                                                                                                                                                             VQVNYVSNVSKSWLLMIQQTEQLSRIMKTHAEDLNSGPLHRLTMMIKDKQQVKKSYVGIH
                                                                                      FAHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHEBMACILKEILQEYLEISSLVQD
                                                                                                                                     QQIEAEMIKYTKTELEKLKSSYRQLIKEMNSAKEKYKEALAKGKETEKAKERYDKATMKL
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  Disclosure; Col 271-274; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prediction; secondary structure; alignment; evolutionary conservation; homology; periodicity; co-variation analysis; antigenic site; site directed mutagenesis; interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY43963 standard;
                                            Predicting the folded structure of proteins
                                                                                           WPI; 1999-570766/48.
                                                                                                                                                                                                                                                                                                                                                                US5958784-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein
                                                                                                                                                                                                                             25-MAR-1992;
                                                                                                                                                                                                                                                                       25-MAR-1992;
                                                                                                                                                                                                                                                                                                                    28-SEP-1999
                                                                                                                                                                                 (BENN/) BENNER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPR-ERVQLLGKRQ 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prediction; secondary structure; alignment; e
homology; periodicity; co-variation analysis;
site directed mutagenesis; interaction.
                                                                    WPI; 1999-570766/48.
                                                                                                                                                                                                                                                                                                                                  25-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Felis catus
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21-DEC-1999
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                                                                                                                                     Benner SA;
                                                                                                                                                                                                                                                                    25-MAR-1992;
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s; antigenic site;
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Predicting the folded structure of proteins

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Disclosure; Col 275-276; 113pp; English
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Sequences AAY43902-Y44015 represent proteins used in a novel method of predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure, active sites, and parsing segments. Secondary structural units are assignment by interesting periodicity in the assignments, and assembled into globular form using distance constraints imposed by disulfide bridges, active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein molecule, as guides for site directed mutagenesis studies, and for understanding the interaction of a protein with other molecules. (Updated on 17-OCT-2003 to standardise OS field)

Sequence 262 8

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                                                                                     CIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPEALNYGRYS
                                                                                                                            IVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTLLQMVGDAAAGMEYLESKC
                 YEPGORPSFSTIYOELOSIRKRH 751
                                    CIHRDLAARNCLVTEKNVLKISDFGMSREEADGIYAAS
                                                                                                                IVRLIGVCTOKOPIYIVMELVQGGDFLTFLRTEGARLRMKTLLQMVGDAAAGMEYLESKC
YEPGORPSFSAIYQELQSIRKRH
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                     34.8%;
                                                                                                                                                                                          Score 1350.5; DB 2;
Pred. No. 3.5e-92;
4; Mismatches 1;
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                                                                            -GLRQVPVKWTAPEALNYGRYS
                                                                                                                                                                                            Indels
                                                                                                                                                                                                               Length
                                                                                                                                                                                                                262;
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                                                                                             668
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Search completed: March Job time : 176 secs 18, 2005, 15:59:19

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/2/pubpna/US07_
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                                                                                                                                                  /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

11	10	9	8	7	σ	ហ	4	ω	N	_	Result No.
198	201.2	227.2	227.2	271.6	296.2	296.2	326.8	2023.4	2256	2256	Score
8.8	8.9	10.1	10.1	12.0	13.1	13.1	14.5	89.7	100.0	100.0	Query
2955	3875	15297	15297	1779	361	361	449	2889	2674	2674	Query Match Length DB
18	15	17	13	17	15	9	10	16	17	13	B
US-10-384-339C-1	US-10-101-510-525	US-10-660-763-3	US-10-003-295-3	US-10-280-576-19	US-10-121-925-5	US-09-948-802-5	US-09-918-995-1503	US-10-240-965-256	US-10-660-763-1	3 US-10-003-295-1	ID
Sequence 1, Appli	Sequence 525, App	Sequence 3, Appli	Sequence 3, Appli	Sequence 19, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 1503, Ap	Sequence 256, App	Sequence 1, Appli	æ	Description

45	44	43	42	41	40	39	38	37	36	35	34	3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
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# ALIGNMENTS

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APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001183DIV
CURRENT APPLICATION NUMBER: US/10/003,295
CURRENT FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 4
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2674
TYPE: DNA
ROANLISM: Homo sapiens
US-10-003-295-1
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Publication No. US20020168741A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 2256; Conserv
121 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGGCCAGAGC
                                                                132 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT 191
                                                                                                       61 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCCAGCGGGTCAAGAGT 120
                                                                                                                                               72 ATGGGCTTCTCTGAGCTGTGCAGCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG
                                                                                                                                                                       1 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGGCCACGGGGTCCTGCAGCAAATGCAG
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100.0%; Pred. No. 0;
ative 0; Mismatches
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B &	1141 CAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCCCGCCTGTGCTG 1200	
o	081 CAAGAAGCACTGCAGGG	
5 B 8	1021 GAAGAGGAGAACACCCACCCCGGGAGCGGGTGCAGCTGGTGGGGAAGAGGCAAGTGCTG 1080	
S B 8	961 ACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGGAGCTCCGGAAT 1020	
\$ B \$	01 CTGA      72 CTGA	
S B 7	841 GATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGGAGCTCCAGCTGAACGAG 900	
O D &	781 TACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCTGTGTCACGTTC 840	
\$ B \$	721 GTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCCGCATCCAGCCTGAGGCTGAG 780	
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S B 7	601 CACCAGCTCCTGCTGCCGGCCTGCGGTCACTGCAGGACCTGCACGAGGAGGAGATGGCT 660	
S B 7	541 GCTCACCACAACCGCTATGTGCTGGGCGTGCGGGGTGCGGAGCTACACCACCAGCACCAC 600	
S & 7	481 AAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTT 540	
Q B .	421 CAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAG	
Q	361 CAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAGC 420	
Q	301 AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG 360 	
S & &	241 GAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAGGGCCCCTGAGC 300	
Q	181 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAG	
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92 TACCAGGAGCTGCAGAGCATCCGAAAGCGGCATC	22	문
21 TACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCGG 22	222	Ş
32 AGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCCCAGCTTCAGCACCC	22	멅
161 AGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGCACCATC 2220	21	S
72 GAGTTTGTGGAGAAGGGGGGCCGTCTGCCCCAGAGCTGTGTCCTGATGCCGTGTT	21	g
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12 TGGGAGACCTTCAG	211	밁
041 TGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACACGG 2100	20	Ş
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21 GGGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAG 19	192	ð
32 GTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGC	193	밁
61 GTG	186	ð
72 ATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGAACTC	18	밁
01 ATGGAGTAC	18	Ş
2 GAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGCTGC		밁
1 GAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAGCTGCTGCC 18	174	S
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92 CTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCCAGAAGCA	16	닭
21 CTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAG 16	16	á
32 TCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGATC 16	163	D D
61 TCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGAT	15	ð
72 AACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACACACCCCTGGTGGCGCG	15	문
01 AACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAACACCCCTGGTGGCGGTGAAG 15	15	Ş
12 AAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGACGGGG	15	망
41 AAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTGTGGGTGAGCAGATTGGACGGGGG 1:	144	Ş
52 CTGAGCACCCAGCAGCCCTCACCAAGAAGAGTGGTGTTGTCCTGCACAGGGCTGTGCC	145	밁
81 CTGAGCACCCAGCAGCCCCTCACCAAGAAGAAGAGTGGTTGT	138	ð
92 AACCTGTACCGACTGGAAGGGGAAGGCTTTCCTAGCATTCCTTTGCTCATCGACCAC	13	ם
21 AACCTGTACCGACTGGAAGGGGAAGGCTTTCCTAGCATTCCTTTGCTCAI	32	S
32 ACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCC	133	닭
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NULT 2 .10-660-763-1 sequence 1, Application US/10660763

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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOL183DIVI
CURRENT APPLICATION NUMBER: US/10/660,763
CURRENT APPLICATION NUMBER: US/10/660,763
CURRENT FILING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2674
TYPE: DNA
ORGANISM: Homo sapiens
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                      ATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCCTGGCACTGCCTG
                                                                    CCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGGACTTCCTGACCTTCCTCCGCACG
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960 CACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGGAGCTCCCGGAA 101 	Q Qq		S-1
900 GCTGACTGTGGAGAGCGTGCAGCACACGCTGACCTCAGTGACAGATGAGCTGGCTG	Qy	OFINATA: FEAR FILESTAN  OTHER NO. 1 PARTY STATE OF THE ST	AL : Das :
840 CGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGAGCTCCAGCTGAACGA 899	Qy	PRIOR APPLICATION UNMBER: 60/195,106 PRIOR FILING DATE: 2000-04-05 PRIOR FILING DATE: 2000-04-05 PRIOR SEG ID NOS: 276 COFFRANCE DEED DECORPORATE	
780 GTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCTGTGTCACGTT 839	Qy	TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION FILE REFERENCE: PA-0025 PCT CURRENT APPLICATION NUMBER: US/10/240,965 CURRENT APPLICATION NUMBER: US/10/240,965	
720 GGTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCCGCATCCAGCCTGAGGCTGA 779	Qy	APPLICANT: EXTINAMER, Jeffrey J. APPLICANT: SZILHAMER, Jeffrey J. APPLICANT: PORTER, Gordon J. APPLICANT: MIKITA, Thomas APPLICANT MIKITA, Thomas	
660 TIGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGTGCAGGATGA 719	Qy Db	APPLICANT: INCYTE GENOMICS, INC. APPLICANT: SHIFFMAN, DOV APPLICANT: SOMOGYI, Roland APPLICANT: INCYTE Michael M APPLICANT: INCYTE	; All
600 CCACCAGCTCCTGCTGCCGGCCTGCTGCGCTCACTGCAGGACCTGCACGAGGAGATGGC 659	Qy Db	US-10-240-965-256 ; Sequence 256, Application US/10240965 ; Publication No. US20030165924A1 ; Publication No. US20030165924A1	US-10 US-10 ; Sec ; Puh
540 TGCTCACCACAACCGCTATGTGCTGCGCGTGCGGGCTGCGCACCACCACCACCACCACCACCACCACCACCACCACC	Qy	ผั	Db Db
480 CAAAGACAAGGACCATGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTT 539	gg Qy	2232 AGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGCACCATC 2291 2221 TACCAGGAGCTGCAGAGCATCCGAAAGCCGCATCGG 2256	ሪያ ይ
420 CCAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAGCGCAAGTACCAGGAGGCCAG 479	Qy	2172 GAGTTTGTGAGAAAGGGGGCCGTCTGCCCAGAGCGGTGTCCTGATGCCGTGTTC 2231 2161 AGGCTCATGGAGCAGTGCTGGGCCTATGAGCCCAGCGCGAGCTCAGCACCATC 2220	δ 8
360 GCAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAG 419 	Qy	2112 TGGGAGACCTTCAGCCTGGGGGGCCTCCCCCTATCCCAGCCTCAGCAATCAGCAGACACGG 2171 2101 GAGTTGTGGAGAAGGGGGCCGTCTGCCTGCCCAGAGCTGTGCTGATGCCGTGTTC 2160	γ <b>0</b> γ , α
488 CAAGCTGAGCCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTG 547	д	2052 GCCCIIAACIACGGCCGCIACICCICCGAAAGCGACGIGIGGAGCIIIGGCAICIIGGC 2110 2041 TGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACACGG 2100 	S S
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181 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT 240	δλ		Db

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Sequence 5, Application US/09948802
Publication No. US20020172981A1
GENERAL INFORMATION:
APPLICANT: ROBISON, KEITH E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND

RESULT 5 US-09-948-802-5

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Sequence 1503, Application US/09918995
; Sequence 1503, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTITILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
; CURRENT APPLICATION UMMER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FASESEQ for Windows Version 3.0
; SEQ ID NO 1503
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; OTHER INFORMATION: n =
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Best Local Similarity
Matches 328; Conserv
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
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FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/09/948,802
; CURRENT FILLING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/387,212
PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NO5: 18
; SOFTWARE: PATENTIN VET: 2.0
; SEQ ID NO 5
; SEQ ID NO 5
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                                             ; OTHER INFORMATION: All US-10-121-925-5
                                                                SEQ ID NO 5
LENGTH: 361
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Query Match
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ORGANISM: Homo sapiens
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 13.1%; ilarity 97.4%; Conservative
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Pred. No. 1.9e-64;
0; Mismatches 4;
 Score 296.2; DB 1
Pred. No. 1.9e-64;
0; Mismatches 4
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RESULT 7

US-10-280-576-19

Sequence 19, Application US/10280576

Publication No. US20040044405A1

GENERAL INFORMATION:

APPLICANT: WOLFE, Matthew R.

TITLE OF INVENTION: VASCULAR STENT OR GRAFT CO/

FILE REFERENCE: 09820.189

CURRENT APPLICATION NUMBER: US/10/280,576

CURRENT FILING DATE: 2002-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-280-576-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/343,732
PRIOR FILING DATE: 2001-10-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 17
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                            GGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAACACCCCTGGTGGCGGTGAAGTCTTGT
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                                                                                                                 CGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGGATCCTGAAG
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Sequence 3. Application US/10003295
; Publication No. US20020168741A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; SEQ ID NO 3
; SEQ ID NO 3
; CRANISM: Homo sapiens
US-10-003-295-3
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US-10-003-295-3
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                                                                  ATGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG
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                                                                                                                                  Conservative
                                                                                                                                              10.1%;
                                                                                                                                <u>,</u>
                                                                                                                              Score 227.2; DB 13;
Pred. No. 7.3e-47;
0; Mismatches 8;
                                                                                                                                8; Indels 152; Gaps
                                                                                                                                                            Length 15297;
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US-10-660-763-3

US-10-660-763-3

; Sequence 3, Application US/10660763

; Publication No. US20040063130A1

; GENERAL INFORMATION:

APPLICANT: GAN, Weiniu et al.

APPLICANT: GNAN, Weiniu et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND

TITLE OF INVENTION: THEREOF

FILLE OF INVENTION UNMER: US/10/660,763

CURRENT APPLICATION NUMBER: US/10/660,763

CURRENT FILING DATE: 2003-09-12

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 15297

TYPE: DNA

ORGANISM: Homo sapiens

US-10-660-763-3
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Best Local Similarity
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                                                                                                                                      GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT
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                                                                    GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGGCCAGAGC 2742
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                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                       10.1%;
                                                                                                                                                                                                                                                                     Score 227.2; DB 17; Length 15297; Pred. No. 7.3e-47; 0; Mismatches 8; Indels 152; Gaps
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APPLICANT: WAN, JACKSON
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 525
LENGTH: 3875
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; ORGANISM: Homo sapiens
US-10-101-510-525
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US-10-101-510-525
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Best Local Similarity
Matches 423; Conserv
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                                                                                                                              TGGGCCAGTTTAGCCACCCGCATATTCTGCATCTGGAAGGCGTCGTCACAAAGCGAAAGC
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nilarity 54.9%;
Conservative
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Pred. No. 2e-40;
0; Mismatches 338;
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PRIOR APPLICATION NUMBER: DE 10100586.5
PRIOR FILING DATE: 2001-01-09
PRIOR PELING DATE: 2001-01-09
PRIOR PELING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: DE 10158411.3
PRIOR REILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: DE 10160151.4
PRIOR APPLICATION NUMBER: DE 10160151.4
PRIOR PILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: HOMO BAPIEDS
; PUBLICATION INFORMATION:
; TITLE: EPh A1
; PATENT DOCUMENT NUMBER: NM00532
US-10-384-339C-1
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US-10-384-339C-1
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                                                                                                                                                          Matches 421;
                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kreutzer, Roland
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: 20200/2002
CURRENT APPLICATION NUMBER: US/10/384,339C
CURRENT FILING DATE: 2003-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/EP02/00152
PRIOR FILING DATE: 2002-01-09
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                                   AAGTGTTCAGCGGACGCCTGCGAGCC-----GACAACACCCTGGTGGCGGTGAAGT 1561
                                                                             GGGAGCTTGATCCAGCGTGGCTGATGGTGGACACTGTCATAGGAGAAGGAGAGTTTGGGG
                                                                                                          GGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGACGGGGGAACTTTGGCG
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milarity 54.7%;
Conservative
                                                                                                                                                        Score 198; DB 18;
Pred. No. 1.3e-39;
0; Mismatches 340;
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; LENGTH: 3370
; TYPE: DNA
; ORGANISM: HOMO 6
US-09-967-768A-144
                                                                                                                                   FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 325
NUMBER OF SEQ ID NOS: 325
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US-09-967-768A-144
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                                                                                        SOPTWARE: PatentIn version 3.0 SEQ ID NO 144 LENGTH: 3370
                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene
TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                                                                                                                                Sequence 144, Application US/09967768A Patent No. US20020150877A1
Query Match
Best Local Similarity
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APPLICANT: MacBeth, Kyle J.
APPLICANT: Teai, Fong-Ying
APPLICANT: Lesoon, Andrea
APPLICANT: Lesoon, Andrea
APPLICANT: Lightcap, Eric S.
APPLICANT: Milliamson, Mark
APPLICANT: Milliamson, Mark
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: LESOON, AND LAURA A.
APPLICANT: LESON, AND LE
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US-10-354-358-101 RESULT 13

Sequence 101, Application US/10354358 Publication No. US20030157082A1 GRMERRAL INFORMATION: APPLICANT: Millennium Pharmaceuticals,

APPLICANT:

Hunter, John Joseph MacBeth, Kyle J Tsai, Fong-Ying Lesoon, Andrea

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UB-10-660-7,

1634, 68862, 9011, 14031, 6178, 21225, 1420, 3230, 1586, 9943,

1634, 68862, 9011, 14031, 6178, 21225, 1420, 3236, 2099,

1634, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,

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Best Local Similarity
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LENGTH: 3370
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PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/389,395
PRIOR FILING DATE: 2002-06-17
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ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (94)...(3048)
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TGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCCGAGAGGAAGCCCGATG
                                                                        TGAACTACCTCAGTAATCACAATTATGTCCACCGGGACCTGGCTGCCAGAAACATCTTGG
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Pred. No. 1.3e-39;
0; Mismatches 340;
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TGAATCAAAACCTGTGCTGCAAGGTGTCTGACTTTGGCCTGACTCGCCTCCTGGATGACT

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; SOFTWARE: PatentIn version 3.2; SEQ ID NO 19; LENGTH: 3370; TYPE: DNA; ORGANISM: Homo sapiens US-10-210-120-19
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PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US 60/334,468
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 123
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Best Local Similarity 54.7%;
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TITLE OF INVENTION: Expression Profile of Prostate
FILE REFERENCE: UM-07221
CURRENT APPLICATION NUMBER: US/10/210,120
CURRENT FILING DATE: 2002-08-01
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                               AGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGCTGGCA
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Pred. No. 1.3e-39;
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RESULT 15
US-10-776-827-82
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; Publication No. US20040132086A1
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 82
LENGTH: 3370
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CURRENT FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: US/09/814,915
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/214,870
PRIOR FILING DATE: 2000-06-28
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APPLICANT: Richer, Jennifer
TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
TITLE OF INVENTION: Thereto
FILE REFERENCE: 2848-39
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RESULT 2
US-10-003-295-1
US-10-003-295-1

Sequence 1, Application US/10003295

Patent No. 6886187

Patent No. 6886187

FERENAL INFORMATION:
APPLICANT: GAN, Weiniu et al.
APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILLE OF INVENTION INTEREOF
FILLE REFERENCE: CL001183DIV
CURRENT APPLICATION NUMBER: US/10/003,295
CURRENT APPLICATION NUMBER: US/10/003,295
CURRENT FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2674
TYPE: DNA
CRGANISM: Homo Bapiens
US-10-003-295-1
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1992 GGGGTCTATGCAGCCTCAGGGGGCCTCTGCACAAGTCCCCAAGCTGTTGACTTCGAACTCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGAACTTTGGCATCTTGCTCTCGAAAAGTGAACTTTGGCATCTTTGCTCTCTCGAAAAGTGAACTTTGGCATCTTTGCTCTCTCT		1561 1632 1621 1692 1681 1752	Db 1392 AACCTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCACACCCTGGTGAAG 1560  Db 1391 CTGAGCAGCCAGCAGCCCTCACCAAGAAGAGTGTTTCCTTGCTCATCGACCACCTA 1451  Db 1452 CTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGTTTGTCCTGCACAGGGCTGTGCCC 1440  Db 1452 CTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGTTTTTGTCCTGCACAGGGCTGTGCCC 1511  Oy 1441 AAGGACAAGTGGGTGCTGAACCATGAGAACCTGGTGTTTGGGTGAGCAGATTGGACGGGGG 1500  Db 1512 AAGGACAAGTGGTGCTGAACCATGAGGACCTTGGTTTGGGTGAGCAGATTGGACGGGGG 1571  Oy 1501 AACTTTGGCGAAGTTGTTCAGCGGACGCCTGCGAGCAACACCCTTGGTGGCGGTGAAG 1560  1572 AACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCACAACACCCTTGGTGGCGGTGAAG 1631	Oy 1021 GAAGAGGAGAACACCCACCCCGGGAGCGGGTGCAGCTGCTGGGCAAGAGGCAAGTGCTG 1080

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                                                                                                                                                                                RESULT 4
Sequence 5, Application US/09948802
Patent No. 6465232
GENERAL INFORMATION:
APPLICANT: ROBISON, KEITH B.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR FILE REFERENCE: MNI-090
CURRENT APPLICATION NUMBER: US/09/948,802
CURRENT FILING DATE: 2001-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/387,212A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
LENGTH: 361
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09387212A Patent No. 6309849
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Best Local Similarity
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TITLE OF INVENTION: NUCL
TITLE OF INVENTION: PHOS
FILE REFERENCE: MNI-090
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NUCLEIC ACID MOLECULES
PHOSPHATASE HOMOLOGUES
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Pred. No. 6e-56;
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; PRIOR APPLICATION NUMBER: 09/387,212
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 5
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE: OTHER INFORMATION: All occurences of n indicate any US-09-948-802-5
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US-09-817-180-3
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Sequence 3, Application US/09817180

Patent No. 6340584

GENERAL INFORMATION:
APPLICANT: GAN, Weiniu et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001183

CURRENT APPLICATION NUMBER: US/09/817,180

CURRENT FILING DATE: 201-03-27

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASTSEQ for Windows Version 4.0
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Best Local
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Best Local (
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                                                                                                                                                                                                                       LENGTH: 15297
TYPE: DNA
                                                                                                                                                                                                        ORGANISM: Human
                                                                                                                                             Local Similarity
 2623
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                   61 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCCAGCGGGTCAAGAGT
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                                                                                                                         Score 227.2; DB 3;
Pred. No. 3.1e-40;
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Pred. No. 6e-56;
0; Mismatches
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Sequence 3, Application US/10003295

Patent No. 6686187

Patent No. 6686187

GENERAL INFORMATION:

APPLICANT: GAN, Weiniu et al.

ITITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001183DIV

CURRENT FILING DATE: 2001-12-06

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 15297

TYPE: DNA

ORGANISM: Homo sapiens
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Best Local Similarity
Matches 394; Conserv
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CGGGCCATCAGCCCTGACAGCCCCCATCAGTCAGGTGGGTCTCTATGGGACTCTGGTGGGT
                               CGGGCCATCAGCCCTGACAGCCCCATCAGTC-----
                                                                                  GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGGCCAGAGC
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                                                                                                                                                                                                                                                               Score 227.2; DB 4; Length 15297; Pred. No. 3.1e-40; 0; Mismatches 8; Indels 152;
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Sequence 12110, Application US/09949016

Sequence 12110, Application US/09949016

GENERAL INFORMATION:
APPLICANT: VENUTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 12110
LENGTH: 19152
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Best Local Similarity
Matches 213; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                                      tch 9.4%; Score 213; DB 4; 1 al Similarity 100.0%; Pred. No. 4.4e-37; 213; Conservative 0; Mismatches 0;
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                                                                                                                                                            GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCCAGCGGGTCAAGAGT
                      CGGGCCATCAGCCCTGACAGCCCCATCAGTCAG 213
                                                                                                   GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC 180
                                                                                                                                                                                   GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT
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  CGGGCCATCAGCCCTGACAGCCCCCATCAGTCAG 18953
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RESULT 8 US-09-949-016-15795

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US-09-814-915A-82
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US-09-949-016-15795
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Horwitz, Kathryn
APPLICANT: Richer, Jennifer
TITLE OF INVENTION: Progesterone Receptor-Regulated Gene
TITLE OF INVENTION: Thereto
FILE REFERENCE: 2848-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version
SEQ ID NO 15795
LENGTH: 19153
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 82, Application US/09814915A Patent No. 6750015
                                                                            Query Match
Best Local Similarity
                                                                                                                                                                          SEQ ID NO 82
LENGTH: 3370
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Best Local Similarity
                                                             Matches 421;
                                                                                                                               -09-814-915A-82
                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/814,915A CURRENT FILING DATE: 2002-03-21 PRIOR APPLICATION NUMBER: 60/214,870 PRIOR FILING DATE: 2000-06-28
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn versio
                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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 GGGAGCTTGATCCAGCGTGGCTGATGGTGGACACTGTCATAGGAGAAGGAGAGTTTGGGG
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100.0%; Pr
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                                                            Score 198; DB 4; Length 3370;
Pred. No. 5.2e-34;
0; Mismatches 340; Indels
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GENERAL INFORMATION:
GENERAL INFORMATION:
FITTLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER
CURRENT APPLICATION NUMBER: US/09/349,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 628
LENGTH: 3921
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US-09-949-016-628
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ORGANISM: Human
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Sequence 2120, Application US/09949016

PATENT NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES AS:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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Pred. No. 3.3e-31;
0; Mismatches 311;
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; SEQ ID NO 2120
; LENGTH: 3921
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2120
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US-09-949-016-5662
; Sequence 5662, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
GENERAL INFORMATION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT APPLICATION NUMBER: 60/241,755
pRIOR APPLICATION NUMBER: 60/241,755
pRIOR FILING DATE: 2000-10-20
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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PastSEQ for Windows Version 4.
; SEQ ID NO 5662
; LENGTH: 3386
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5662
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                                                                                                 US-08-357-642A-2
                                                                                                                     RESULT 13
                                              Sequence 2, Application US/08357642A Patent No. 5837524 GENERAL INFORMATION:
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Best Local Similarity 54.7%;
Matches 392; Conservative
APPLICANT: Sima Lev
APPLICANT: JOSEPH Schlessinger
TITLE OF INVENTION: PYK2 RELATE
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 PYK2 RELATED PRODUCTS
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Pred. No. 7.5e-29;
0; Mismatches 319;
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 1918 GATGGGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCT
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; TYPE: nucleic acid
; STRANDENNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic
US-08-357-642A-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3416
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NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
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APPLICATION NUMBER: US
FILING DATE: December
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MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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STREET: 633 West Fifth
STREET: Suite 4700
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STATE: California
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392; Conserv
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                                       CTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCC
                                                                                    GCCATGGCCTACCTGGAGAGCATCAACTGCGTGCACAGGGACATTGCTGTCCGGAACATC
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Pred. No. 7.5e-29;
0; Mismatches 319;
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Patent No. 5837815
GENERAL INFORMATION:
                                                           Query Match
Best Local Similarity
Matches 392; Conserv
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMEER: 08/357,64:
FILING DATE: December 15, 199-
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,77
REFERENCE/DOCKET NUMBER: 21/:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                            TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: BCOTAGE
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APPLICATION NUMBER: US
FILING DATE: June 2, 1
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TITLE OF INVENTION: PYK-2 RELATED PRODUCTS
TITLE OF INVENTION: METHODS
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STREET: Suite 4700
CITY: Los Angeles
STATE: California
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                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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                                                               Score 174.6; DB 2;
Pred. No. 7.5e-29;
0; Mismatches 319;
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US-09-016-434-1483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1483, Application US/09016434 Patent No. 6500938
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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3174 PORTER DRIVE
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:

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; TOPOLOGY: linear;; IMMEDIATE SOURCE:; LIBRARY: GENBANK; CLONE: 9988304
US-09-016-434-1483
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELECHONE: (650) 855-0555
TELECAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1483:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 392; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION:
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2158 TTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGC 2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1476 AAGACCTGCAAGAAAGACTGCACTCTGGACAACAAGGAGAAGTTCATGAGCGAGGCAGTG
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                                                                      2010 ATCGGGGTGCTGGAGAAAGGAGCCGGCTGCCCAAGCCTGATCTCTGTCCACCGGTCCTT 2069
                                                                                                  CGGGAGTTTGTGGAGAAAGGGGGGCCGTCTGCCCCTGCCCCAGAGCTGTTCCTGATGCCGTG 2157
                                                                                                                                                                        CTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACA 2097
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> Search completed: March 19, Job time: 373.746 secs 2005, 14:24:17

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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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13179.075 Million cell updates/sec
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gb_gss2:*
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21.1	21.9	22.0	22.1	22.1	22.4	22.9	22.9	23.3	23.4	24.3	24.4	25.3	25.3	25.5	25.5	25.5	25.8	26.0	26.5	26.6
600	732	748	643	582	573	675	805	943	580	674	662	787	1077	638	912	782	812	911	938	962
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ALIGNMENTS

## REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 CR624741 LOCUS DEFINITION Ś REFERENCE ORIGIN FEATURES COMMENT TITLE JOURNAL REMARK Query Match Best Local Similarity Matches 2131; Conserv JOURNAL TITLE AUTHORS source Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2461) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished μ - Web: www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. Homo sapiens (human) CR624741 2461 bp mRNA linear full-length cDNA clone CSODI069YK21 of Placenta Cot of Homo sapiens (human). CR624741.1 GI:50505548 HTC; CNSLT\_cDNA. Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr Genoscope Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 CR624741 Direct Submission Faraday Avenue ATGGGCTTCTCTGTAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG (bases 1 to 2461) Conservative /organism="Homo sapiens" /mol type="mRNA" /db\_xref="taxon:9606" /clone="CSODIO59YK21" /tissue\_type="Placenta Cot 2 /plasmid="pCMVSPORT\_6" 1. .2461 Location/Qualifiers 76.8%; .. Score 1732.8; Pred. No. 0; Mismatches 25-normalized" DB 3; 2; Indels Length 2461; 377; Gaps HTC 21-JUL-2004 25-normalized 60

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Query Match  44.4%; Score 1002; DB 3; Length 1189;  Best Local Similarity 100.0%; Pred. No. 1.2e-200;  Matches 1002; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  1255 GGAAGGACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAG 1314	rce	BP 191 91006 EVRY cedex - FRANCE (E-mail: - Web: www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligend enriched, double-strand cDNA was digestinto the Not I and EcoR V sites of the pCMV was normalized. Library was constructed by	Attp://rulliength.invitrogen.com/ invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1189) Genoscope. Direct Submission Submitted (20-HH-2004) Genoscope - Centre National de Semiencage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 1189) 1 (bases 1 to 1189) 11. Hength cDNA libraries and normalization Unpublished Contact: Feng Liang Email: fliang@lifetech.com URL:	of Homo sapiens (human).  1 CR593957  CR593957  CR593957. GI:50474764  HTC: CNSLT_cDNA.  Homo sapiens (human)	CR593957 1189 bp mRNA linea	2207 GCTTCAGCACCATCTACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCGG 2256	2147 CTGATGCCGTGTTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGGCCCA 2206	2087 ATCAGCAGACACGGGAGTTTGTGGAGAAGGGGGCCGTCTGCCCTGCCCAGAGCTGTGTC 2146	2278 2277	2252 GGACCGCACCTGAGGCCCTTAACTAC. 2277 2027 TTGGCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCA 2086	
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(L) Unpublished (2001)
(D) May 5, 2003 this sequence version replaced gi:30372027.
(Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPRT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                       GCTGGCATGGAGTACCTGGAGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTCGGAAC
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/mol_type="mRNA"
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High-efficiency full-length cDNA cloning
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Please visit our web site (http://genome.gsc.riken.jp/) for further contails.
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3373)
GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC
                                                                              GAGGCCGAGCTTCGTCTACTGGAGGGGCATGAGAAAGTGGATGGCCCCAGCGGGTCAAGAGT
                                                                                                                                                 ATGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG
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                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="lung"
/clone_Tib="RIKEN full-length enriched mouse
/dev_stage="adult"
1. .3373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="FANTOM_DB:1200003015"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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     CAAGAGGCAGATGCTGCAAGAGGCAATACAAGGGTTGCAGATAGCACTGTGCAGCCAGGA
                                                                          GCGTGAGCTCCAAAGTGAGGAACAGAACACCCCCCCCGGGAACGGGTGCAGCTTCTGAG
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900 951 840 891 780 831 720 771 660 711 600 651 540 591 480

Query Matches Matches Qy Db Dy	ORIGIN	FEATURES	VERSION KEYWORDS SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 5 AL542976 LOCUS DEFINITION ACCESSION	B & 8		
Ouery Match 37.6%; Score 848.8; DB 1; Length 936; Best Local Similarity 99.2%; Pred. No. 2.5e-168; Matches 861; Conservative 2; Mismatches 4; Indels 1; Gaps 1;  1 ATGGGCTTCTTCTTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 60	Litte Con Con Con Con Con Con Con Con	Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: segref@genoscope.cns.fr, Web:: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pcMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7663.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODE013DH01QP1&c=7663.f. Location/Qualifiers	-3	AL542976 AL542976 Hom 5-PRIME, mRN AL542976			1125 CAAGCTGCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGA 1184
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Plate: LLMN12347 row: b column: 05
High quality sequence stop: 704.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/lab host="PH108 (phage-resistant)"
/clone lib="NIH_MGC 92"
/note="Torgan: testis; vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:5583652"
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
18t strand cDNA was primed cDNA was digested with Not I and cloned
18t end enriched, double-strand cDNA was digested with Not I and cloned
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On May 5, 2003 this sequence version replaced Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO51BH10QP1&c=7663.f. Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC
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                                                                                                                                                              GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT
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                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Tst trrand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI051Y020"
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M Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrai
Mammalia; Eutheria; Primates; Catarrhini; Homini;
1 (bases 1 to 939)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi
Contact: Genoscope
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              ACACCAGCTCCTGCTGCCGGCCTGCTGCGGTCACTGCAGGACCTGCACGAGGAGATGGC
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremteux, CP 5706 - $1057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr. Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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/mol_type="mRNA"
/db_xref="taxon:9606"
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1 (bases 1 to 948)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (1)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson
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BQ708270.1
EST.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCMZ516 row: o column: 07
High quality sequence stop: 610.
Location/Qualifiers
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                                                                                                                                  Conservative
                                                                                                                                                                                                       /lab host="NHIOB (phage-resistant)"
/Clone_lib="NHIM_MGC_113"
/Clone_lib="NHIM_MGC_113"
/Clone_lib="NHIM_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EccRI; cDNA made by oligo-dT priming. Directionally cloned into EccRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubbin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6301278"
                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
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                                                                                                                                            Score 771.6; DB 5;
Pred. No. 4.8e-152;
                                                                                                                                  Mismatches
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
On May 5, 2003 this sequence version replaced Contact: Genoscope
Genoscope - Centre National de Sequencage
                                                                                                                                                                           BX356088 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO08YG07 3-PRIME, mRNA sequence.

BX356088 BX356088 BX356088 CI:46288403

EST.
                                                                                                                                               Homo sapiens
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 980)
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Location/Qualifiers
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CCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAGTGCTG
                                                                                 GGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACACGGGAGTTTGTGGAGAAGGGGGG
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                                                     GGCCTCCCCTATCCCAACCTCAGCAATCAGCAGACACGGGAGTTTGTGGARAAGGGGGG
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/db_xref="taxon:9606"
/clone="CS0DI008YG07"
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Pred. No. 8.9e-148;
1; Mismatches 8;
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM332 row: C column: 07
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1 (bases 1 to 922)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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922 bp mRNA linear EST 04-SEP-2002
AGENCOURT_8071250 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6090558
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BU156855
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                    AGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTTGCTCACCACAACCGCTATG
                                                                                GGGACAGTGCCCAAGCCAAGCGCAAGTACCAGGAGGCCAGCAAAGACAAGGACCGTGACA
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AGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTTGCTCACCACAACCGCTATG
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/lab host="UPH10B (phage-resistant)"
/clome lib="NIH MGC 112"
/clome lib="NIH MGC 112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI, cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor:
GCCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript I RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6090558"
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AGENCOURT 6492411 NIH_MGC_125
5', mRNA sequence.
EM543870
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1114)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                             TGCAGCTGCCTGCCCGCATCCAGCCTGAGGCTGAGTACCAAGGCTTCCCTGCGACAGTATGG
                                                                                                                                                  ATACCTGGAGATTAGCAGCCTGGTGCAGGATGAGGTGGTGGCCATTCACCGGGAGATGGC
                                                                                                                                                                                                                     GCGGTCACTGCAGGACCTGCACGAGGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGA
                                                                                                                                                                                                                                                                                             CGTGCGGGCTGCCAGCACCACCAGCACCACCAGCTGCTGCTGCCCGGCCTGCT
                                                                                                                                                                                                                                                                                                                                                                     GGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGG
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                                                                                                                             ATACCTGGAGATTAGCAGCCTGGTGCAGGATGAGGTGGTGGCCATTCACCGNGAGATGGC
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/db_xref="taxon:9606"
/clone="IMAGE:5589213"
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Pred. No. 3.6e-139;
0; Mismatches 27;
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found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM12361 row: i column: 22 High quality sequence stop: 566.
                                                                                                                          /clone lib="NIH MGC_125"
//clone lib="NIH MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site 1: ECORV (destroyed); Site 2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(ECORV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."
Length
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9

Gaps

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REFERENCE
AUTHORS
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VERSION
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                                                                                                                                                                              Query Match
Best Local Similarity
Matches 716; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agancourt Bloscience Corporation

Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 847)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: LLCM2326 row: o column: High quality sequence stop: 721. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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               AGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTTGCTCACCACAACCGCTATG
                                                                                        TCACCAAGACCCACAGCCAGGACATTGAGAAAGCTGAAGAGCCAGTACCGAGCTCTGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCACACGCCTGACCCTCATTGACCAATGAGCTTGGCTGTGGGCACCGAAA
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                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                  /tissue_type="melanotic melanoma, cell line"
/lab host="DH10B (phage-resistant)"
/clome_libe="NIH MGC_112"
/clome_libe="NIH MGC_112"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6088554"
                                                                                                                                                                                             31.2%;
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                                                                                                                                                                                             Score 703.2; DB 5;
Pred. No. 1.3e-137;
                                                                                                                                                                                Mismatches
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            BX359009.2 GI:46305682
                                                                                                                                                                                                                                                                                                                                                                                                                                           BX359009
                                                                        Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 989)

Li, Wals, Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30376296.

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                        Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 989 bp mRNA linear EST 08-APR-2000
BX359009 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI051Y020 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                               For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO51BH10NP1&c=7663.f.
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/db_xref="taxon:9606"
/clone="CSODI051Y020"
tissue_type="PLACENTA COT 25-NORMALIZED"
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RESULT 15
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Best Local Similarity
Matches 787; Conserv
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BX327963 973 bp mRNA linear EST 07-APR BX327963 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens clone CSODI069YK21 5-PRIME, mRNA sequence.
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/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR '
sites of the pCMVSPORT 6 vector. Library was normalized
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Pred. No. 2e-136;
3; Mismatches 13;
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Best Local Similarity
Matches 695; Conserv
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BX327963.1
EST.
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 973)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAGO35ZCO9_CSO3331_1&c=7663.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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CCCCCGGGAGCGGGTGCAGCTGCTGGGCAAGAGGCAAGTGCTGCAAGAAGCACTGCAGGG 1097
                                                                                                                                                                                   GCAGCACACGCTGACCTCAGTGACAGATGAGCTGGCTGTGGCCACCGAGATGGTGTTCAG
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                                                                                             GCGGCAGGAGATGGTTACGCAGCTGCAACAGGAGCTCCGGAATGAAGAGGAGAACACCCCA
                                                                                                                                                               GCAGCACACGCTGACCTCAGTGACAGATGAGCTGGCTGTGGCCACCGAGATGGTGTTCAG
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                                                                                                                                                                                                                                                                                     GGAGGGTGAACCGCTGGAGCCTGGGGGAGCTCCAGCTGAACGAGCTGACTGTGGAGAGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="PLACENTA COT 25-NORMALIZED" /clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED" /clone="Ist strand cDNA was primed with a NotI-oligo(dT) primer rive prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI069YK21"
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Search completed: March 19, 2005, 14:10:46 Job time : 6521.86 secs	1277 TCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAGTTCTCG 1320	1218 CCACTCCACGTCGTCCTCGGAGCAGGAGCGAGAGGG-GGGAAGGACACCCACGCTGGAGA 1276	1158 CAAGCTGGAGCACCTGGGCCCCGGCGAGGCCCCGCCTGTGCTGCTGCTGCAGGATGACCG 1217	1098 GCTGCAGGTAGCGCTGTGCAGCCAGGCCAAGCTGCAGGCCAGGAGTTGCTGCAGAC 1157

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: geneseqn1990s:*
3: geneseqn2000s:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AAS17052

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ABL18403
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AAS95001
ADR39816
ADH43089
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Abv75413 Human kin
Adm28580 Human pro
Adk71888 Human kin
Aa895001 Human NA
Adr39816 Human NA
Adr39816 Human kin
Adh43089 CRAM prot
Aan70060 fes/fps p
Adl71052 Gene enco
Add7298 Novel can
Adl71052 Gene enco
Ach14291 Human pro
Aba14950 Human pro
Aba461604 Human pro
Aba519765 Drosophil
Ab114457 Drosophil
Ab14457 Drosophil
Ab144501 Human pro
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8.2	8.2	8.2	8.2	8.2	8.2	8.2	8.2	8 . 2	8.8	8.8	8.8	8.8	8.8	8 8	8.8	8.8	8. 8	8.8	8.8	8.8	8.9	8.9	10.0	10.1
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Adb37439 Human can	Abz34865 Coding se	Abv94231 Breast ca	Acn37278 Tumour-as	Acn42099 Human dia	Ab191659 Human pol	Abx09937 Human eph	Abz35694 Human eph	Human		Marker	Ade38440 Human pro	Add18447 Human pro	Abz34861 Coding se	Abl67952 Ovary can	Ab191658 Human pol	Abx09936 Human eph		Abv78117 Human eph	Adp28218 Human sec	Ade08824 Novel DNA	Abz35414 Human gen	Adk71885 Human kin	Abk84514 Human cDN	Adm28582 Human pro

## ALIGNMENTS

ABA94500 standard; cDNA; 2674 BP

ABA94500;

09-APR-2002 (first entry)

Human proto-oncogene tyrosine kinase encoding cDNA.

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RESULT 1
ABA94500
ID ABA94500
ID ABA94500
ID ABA9
XX ABA9
XX Prot
XX CDS
FT CDS
FT S'UI
FT 3'UI
FT GDS
XX Y
XX PROT
XX PP 27-M
XX X PP 27-M
XX Y
XX PP 27-M
XX Y
XX WPI;
DR WR P-PK
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             Nucleic acids encoding a proto-oncogene tyrosine kinase, useful for the prevention, diagnosis and treatment of e.g. leukemia and lung tumors.
                                                                  WPI; 2002-138497/18.
P-PSDB; ABB07354.
                                                                                                                           Gan W,
                                                                                                                                                                                                                                                                         22-JAN-2002.
                                                                                                                                                                                                                                                                                                           US6340584-B1.
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                                                                                                                           Ye J, Di Francesco V,
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72. .2330
/*tag= b
/product= "proto-oncogene tyrosine kinase"
2331. .2674
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Query Match
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Matches 2256
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oncogene tyrosine kinase (poTK). The poTK polynuclectides and protein may
be used in the prevention, diagnosis and treatment of diseases associated
with inappropriate poTK expression, such as lung and kidney tumours,
leukemia and stomach adenocarcinoma. poTK may be used to treat disorders
associated with decreased expression by rectifying mutations or deletions
in a patient's genome that affect the activity of poTK by expressing
inactive proteins or to supplement the patients own production of poTK.
The encoded poTK may be used as an antigen in the production of
antibodies against poTK and in assays to identify modulators of poTK
expression and activity. The anti-poTK antibodies and antagonists may be
used to down regulate expression and activity and as diagnostic agents
for detecting the presence of poTK in samples. The present sequence
represents a cDNA encoding the human poTK
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06-DEC-2001; 2001US-00003295
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New human kinase protein, useful for treating or diagnosing disorders associated with an absence of, inappropriate, or unwanted expression of the protein, e.g. inflammation or cancer, in drug screening assays and pharmacogenomics.

Claim 4 (b); Fig 1; 75pp; English.

The invention relates to a newly isolated peptide sequence of a human CC kinase that is related to the proto-oncogene tyrosine kinase subfamily. CC The activity of the kinase of the invention may be described as, CC cytostatic, antiarteriosclerotic, antiinflammatory and antipsoriatic. CC Peptides of the invention are useful in assays to determine the CC biological activity of the protein, in drug screening assays, tissue CC diagnosing disorders characterised by an absence of, inappropriate, or CC unwanted expression of the protein, such as inflammation, cancer (e.g. celakaemia, lung tumours, kidney tumours or stomach adenocarcinoma), CC arteriosclerosis, and psoriasis. Nucleic acid molecules of the invention CC are useful as probes, primers and chemical intermediates in biological cassays. The peptide and nucleic acid sequences are useful as models for the development of human therapeutic targets, aid in the identification cof therapeutic agents that modulate kinase protein activity in cells and clasues that express the protein. The protein of the invention may also be useful in gene therapy. The gene encoding the protein may also compresents the human chromosome 15. The current sequence

Sequence 2674 BP; 662 A; 767 C; 810 G; 435 T; 0 U; 0 Other;

8 밁 S 밁 S 밁 8 맑 8 밁 S á S δ 밁 S Query Match Best Local Similarity Matches 2256; Conserv 541 481 492 421 432 361 372 301 312 241 252 181 192 121 132 61 72 GCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCGCAGCTACACCACCAGCACCAC AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG GACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCCAGAGC GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT GAGGCCGAGCTTCGTCTACTGGAGGCGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGGCCACGGGGTCCTGCAGCAAATGCAG ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG AAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTT CAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAGC GAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGGGATCTGAACTCAGGGCCCCCTGAGC GAGGGCCTGAGCCGCTTGCTGCGGCAGCACCACGAGAGGATCTGAACTCAGGGCCCCTGAGC GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC CAGTACCGAGCTCTGGCACGGGACAGTGCCCAAAGCCGAAGTACCAGGAGGCCAGC **AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG** CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT CGGGCCATCAGCCCTGACAGCCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT Conservative 100.0%; 0 Score 2256; Pred. No. 0; Mismatches 밁 0 œ •• Length 2674; Indels 0 Gaps 600 611 540 551 480 491 420 431 360 371 300 311 240 251 180 191 120 131 6

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                                               GAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAGCTGCTGGC
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                          26-AUG-2002;
25-SEP-2002;
27-SEP-2002;
11-OCT-2002;
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polymorphism; SNP.
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Baughn MR, Richardson TW, Marquis JP, Sw
Becha SD, Emerling BM, Jin P, Wilson AD,
Chang H, Yang YG, Lee SY, Khare R, Elli
Chawla NK, Ramkumar J, Gururajan R, Tribo
                                                                                                                                                                                                         (INCY-) INCYTE CORP
                                                                                                                                                                             P, Swarnakar A, Tang YT;
on AD, Yue H, Gietzen KJ;
Elliott VS, Hafalia AJA;
Tribouley CM, Chien D,
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P-PSDB; 2004-226830/21. DB; ADK71829.

New human kinases and phosphatases, useful for diagnosing, treating preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, car or hepatitis.

Claim 5; SEQ ID NO 65; 347pp; English.

The invention relates to a novel isolated polypeptide which is a human cc kinase and phosphatase (KPP). The polypeptide of the invention cc demonstrates cardiovascular, antiarteriosclerotic, hypotensive, cantintopic, antiantianginal, anti-HIV, antiallergic, corrective, immunosuppressive, antityproid, dermatological, acc antidiabetic, nephrotropic, antigout, gastrointestinal, neuroprotective, corrective, corrective, corrective, antiparatic, opthalmological, antiparatic, crossensian, nootropic, anticonvulsant, hepatotropic, antiparatic, crossensian, reprotozoacide and fungicide activities. The crossensial, virucide, protozoacide and fungicide activities. The crossensial virucide, protozoacide and fungicide activities and crossensial crossensial for diagnosing, treating or preventing crossensial such as cardiovascular diseases, immune system disorders, cell crossensial disorders and viral, bacterial, fungal, parasitic, cell protozoan or helminthic infections. Furthermore, the molecules of the crossensial to model human crossensial canimals to model human crossensial control to the invention.

Sequence 2599 BP; 541 A; 786 C; 828 <u>ი</u> 444 T; 0 U; 0 Other;

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Best Local Similarity
Matches 2253; Conserv 395 301 335 181 155 455 361 241 275 215 121 61 95 GACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGGCCAGAGC GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT ATGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGGCCACGGGGTCCTGCAGCAAATGCAG GAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAGGGCCCCTGAGC GAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAGGGCCCCTGAGC CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT ATGGGCTTCTTCCGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG CAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAGC AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGGCCAGAGC Conservative Score 2206.2; Pred. No. 0; 0; Mismatches <u>.</u> ω --Indels 35; Gaps 480 514 454 360 394 300 334 180 214 120 154 6

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Human; foam cell differentiation; atherosclerosis; cerebral stroke; cardiovascular disorder; coronary artery disease; gene therapy; ds.
                                                                                            Human DNA sequence #256 expressed during foam cell differentiation
                                         Homo sapiens
                                                                                                                 14-FEB-2002
                                                                                                                                      AAS95001;
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Best Local Similarity
Matches 2255; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as atherosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used PCR primers and probes. The polynucleotide sequences can also be used useful in gene therapy. AAS94746-AAS95021 represent the human polynucleotide sequences of the invention which are differentially expressed during foam cell differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell
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human; kinase and phosphatase protein; KPP; enzyme; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;
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Query Match Best Local S Matches 2078

Similarity

Conservative

<u>,</u>

4.

Indels 384; Gaps

Score 1671.6; DB 13; Pred. No. 1.1e-305; Mismatches

ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGGCCACGGGGTCCTGCAGCAAATGCAG

GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT ATGGGCTTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG

120 154 6 Ŋ Sequence

2623

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541 A; 786 C; 74.1%;

840 G;

456 T; 0 U;

0 Other Length 2623;

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The present sequence encodes the human kinase and phosphatase protein (KPP), designated KPP-43. The human KPP sequences from the present CC invention have cytostatic, antiarreriosclerotic, anticonvulsant, concurrence cytostatic, antiarreriosclerotic, anticonvulsant, control concurrence cytostatic, antiarreriosclerotic, anticonvulsant, control contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-2003; 2003US-0449059P.
19-MAR-2003; 2003US-0456332P.
28-MAR-2003; 2003US-045844P.
09-APR-2003; 2003US-0461678P.
17-APR-2003; 2003US-0463937P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human kinases and phosphatases (KPP) for diagnosing, treating and preventing diseases or conditions associated with aberrant KPP expression e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ramkumar J, Marquis JP, Swarnakar A, Chawla NK, Tran U
Becha SD, Lee SY, Hafalia AJA, Richardson TW, Khare R,
Jackson AA, Yang J, Gorvad AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; SEQ ID NO 89; 299pp; English.
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DB; ADR39770.
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B &	D	₽ <i>Q</i>	D &	Qy Db	g Q	Qy db	D QY	D 29	D Q	g 9	g Q	g 49	B 5	} B	S B	. <i>S</i>	Db Qy	dg Vo	문
2011 AGCAAGTGTGAAGCTTTGGCATCTTGCTCTGGGAAGACCTTCAGCCTGGGGGGCCTCCCCC 2200 2141 AGCGACGTGTGGAGCTTTGGCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCCCCC 2200	CAAGTICCCCGTGAAGTIGGACCGCACCTGAGGCCCTTAACTACGCCGCTACTCCTCCGGAA			1771 CTGCAGATGGTGGGGATGCAGCTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATC 1830 	1711 GGGGGCGACTTCCTGACCTTCCTCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTG 1770	1651 CGTCTCATTGGTGTCTGCACCCAGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAG 1710 	1591 AAGGCCAAGTTTCTACAGGAAGCGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTG 1650 	1531 CGAGCCGACAACACCCTGGTGGCGGTGAAGTCTTGTCGAGAGACGCTCCCACCTGACCTC 1590	1471 CTGGTGTTGGGTGAGCAGATTGGACGGGGGAACTTTGGCGAAGTGTTCAGCGGACGCCTG 1530	AGTGGTGTTGTCCTGCACAGGGCTGTGCCCAAGGACAAGTGGGTGCTGAACCATGAGGAC	CTAGCATTCCTTGCTCATCGACCACCTACTGAGCACCCAGCAGCCCCTCACCAGGAGCCCCTCACGAGACCCCTCTGAGCACCCAGCAGCACCCAGGAGCACCCAGGAGCACCCAGGAGCACCCAGGAGCACCCAGGAGCACCCAGGAGCACCCAGGAAGCACCCAGGAGCACCCAGGAAGCACCCAGGAGCACCCAGGAAGAA	CCCCGGCACTTCATCCAGTCCTTGGATAACCTGTACCGACTGGAAGGGGAAGGCTTT	CTGGTGCGGGAGAGCCAGGGCAAGCAGGAGTACGTGCTGTCGGTGCTGTGGGATGGTCTG	1301 TACCACGGGGCCATCCCGAGGGCAGAGGTGGCTGAGCTGCTGGTGCACTCTGGGGACTTC 1360	1241 CTCCCTCCACCGCTGCAGCTCATTCCGGAGGTGCAGAAGCCCCTGCATGAGCAGCTGTGG 1300		1261 ACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCCAAGTTCTCG 1320	1201 CTCCTGCAGGATGACCGCCACTCCACGTCGTCCTCGGAGCAGGAGCGAGAGGGGGGGAAGG 1260	1061 CAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCCCCGCCTGTGCTG 1120

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RESULT 7
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  Query Match
Best Local Similarity
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                                                                                                                       The invention relates to a method for inducing neutralisation of cells or tissues by using a protein binding to CRAM (collapsing-response mediator protein-associated molecule) protein or its encoded gene. The proteins and their encoded genes are useful in gene therapy and regenerative medicine, e.g. by inducing neutralisation of mitochondria. They are also applicable in diagnosis, drug development for neural diseases and studying the mechanism of pathosis. The current sequence represents CRAM protein related cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuroprotective; neutralisation; CRAM; collapsing-response mediator protein-associated molecule; mitochondria; drug development; neural disease; pathosis;
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P-PSDB; ADH43090.
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27-JAN-1991
The fur gene, encoding furin, is in the human and cat genomes directly upstream of this fee/fps proto-oncogene sequence. Furin is strongly expressed in specific types of tumours and labelled RNA or DNA probes of the fur gene and antibodies against furin can be used for diagnostic purposes. (See also ANN70061-62 and AAP70056). (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
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Best Local Similarity
                                                                                                                                                               Osteopathic; antiinflammatory; antirheumatic; antiarthritic; gene therapy; type II collagen; expression; cartilage disease; osteoarthritis; cartilage defect; rheumatoid arthritis; human;
                                                                                                                                                                                                                                                                 Gene encoding type II collagen expression promoting protein,
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tive 0; Mismatches 0;
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Best Local Sim:
Matches 606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New purified protein that promotes type II collagen expression, useful for preventing and treating a cartilage disease, e.g. osteoarthritis, cartilage defect, or rheumatoid arthritis.
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This invention is related to a novel isolated canine nucleic acid sequences and the construction of canine microarrays containing a significant portion of the canine genome. The isolated canine nucleic acid sequences of the invention may be useful for drug screening and toxicity assays. The invention is therefore useful for assessing the impact, including toxicity, of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism. The methods are useful for detecting genes that are up- or down-regulated in canines:
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Best Local Similarity
Matches 368; Conserv
                                                                                                                     Osteopathic; antiinflammatory; antirheumatic; antiarthritic; gene therapy; type II collagen; expression; cartilage disease; osteoarthritis; cartilage defect; rheumatoid arthritis; human;
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Best Local Similarity
Matches 573; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New purified protein that promotes type II collagen expression, useful for preventing and treating a cartilage disease, e.g. osteoarthritis, cartilage defect, or rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2584 BP;
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19-APR-2002;
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DB; ADL71055.
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GGTATGTTGTATCTCGAGAGTAAAAACTGTATACACAGGGACCTTGCTGCAAGAAACTGC
                                                                                                                CAGCCTGTCTACATCATTATGGAACTGGTTTTCAGGAGGTGATTTCCTCACCTTTCTGAGA
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JONES L W.
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The invention relates to an isolated polynucleotide comprising any or 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence determined by the technique of SBH (sequencing by hybridisation). Also

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38043 cDNA sequences, appearing as determined by the technique of SBH included is a purified polypeptide

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (BST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligoners for PCR, for alternating and other traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; 88; protein kinase; mine16676human_81; cytostatic; antianginal; hypotensive; cardiant; cardiovascular disorder; heart failure; hypertension; atrial fibrillation; dilated cardiomyopathy; hypertension; atrial fibrillation; dilated cardiomyopathy; angina; proliferative disorder; cancer;
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   (MILL-) MILLENNIUM PHARM INC
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                                                                          9908-00387212
                                                                                                                                                     9908-00387212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; breast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colon sarcoma;
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The invention relates to identifying a compound which binds to a Kinase (encoded by a nucleotide sequence of 1868, 403, 545, 361, 473, 3001, 526, 663 or 1448 base pair (bp) as given in the specification) comprising contexting the kinase with a test compound under suitable conditions for binding, and detecting binding of the compound to the Kinase. The method cis useful for identifying a compound which binds to the kinase and also for isolating compounds which modify the activity of the kinase. The characterised by aberrant kinase activity where the disorder includes cidentified compounds which modify the activity of the kinase. The condition characterised by a deregulation, e.g. an upregulation or a condition characterised by a deregulation, e.g. an upregulation or a condition characterised by a deregulation, e.g. an upregulation or a condition characterised by a deregulation, e.g. an upregulation or a condition of cellular growth, Cellular growth deregulation of cellular growth, Cellular growth deregulation of cellular growth, cellular growth deregulation, cellular condifferation, at a serial fibrillation, dilated conditions as cancer (including melanoma, prostate cancer, cervical, breast, colon sarcoma). The kinases and antibodies raised against them care useful in one or more method such as screening assays, predictive medicine and methods of treatment. The nucleic acid molecules are useful cor expressing kinase and phosphatase mRNA or a genetic collaboration, the collaboration of the present sequence is a cDNA for a human protein consequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying compound which binds to a Kinase, useful for treating diseases e.g. cancer, by contacting kinase with test compound and detecting its binding to the kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 5; 45pp; English
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Query Match Best Local S Matches 333 Sequence 361 BP; 71 1911 1853 1793 1733 1613 CGAGGATCCTGAAGCAGTACAGCCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCC 1673 260 200 140 80 20 Similarity GGAAGCC---GATGGGGTCTATGCAGCCTCAGGGGGGCCTCAG 1949 TCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAG ACTGCCTGGTGACAGAGAAGAATGTCCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA 1910 CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA 1852 AGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGCGACTTCCTGACCTTCC CNAGGATCCTGAAGCAGCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCC CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA TCCGCACGGAGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAG GGAAGCCCGATTGGGGGGTCTATGCAGCCTCAGGGGGGCCTCAG **ACTGCCTGGTGACAGAGAATGTCCTGAAGAATCAGTGACTTTGGGGATGTCCCGAGA** Conservative 13.1%; A; 101 C; 120 G; 68 T; <u>.</u> Score 296.2; Pred. No. 1.9 Mismatches .9e-46; DB 6; 0 U; 1 Other; Indels Length 361; 5 Gaps 1792 1732 1672 259 199 139 79 w

RESULT 14
AAD61604
ID AAD61
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AC AAD61

standard; cDNA; 361

AAD61604 AAD61604 S 밁 Ś 밁 Ś 밁 S 밁 S 문 Ś

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15-JAN-2004 (first entry)

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RESULT 15
ABX14976
ID ABX14
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AC ABX14
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Best Local Sim
Matches 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method for detecting the presence kinases or phosphatases encoded by nucleotides. The kinases and phosphatases and their encoding nucleic acids are potentially useful drug targets. The present invention may also be useful in diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-AUG-1999; 99US-00387212
07-SEP-2001; 2001US-00948802
13-MAR-2003
                          ABX14976;
                                                  ABX14976 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 361 BP; 71 A; 101 C; 120 G; 68 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting and modulating the activity of specified kinases phosphatases which are potentially useful as drug targets.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein kinase cDNA, 16676S1.
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                                                                                                                                                                                                                                                                                                                                                                                                  CGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCAATTGGTGTCTGCACCC
                                                                                                                                                                                                                                                                                                                                              Fig 5; Opp; English.
                                                                                                                                                                                    ACTGCCTGGTGACAGAGAAGAATGTCCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA 1910
                                                                                                                                                                                                                                       CTGCTGGCATGGAGTACCTGGAGAGAGAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA
                                                                                                                   GGAAGCCCGATTGGGGGGTCTATGCAGCCTCAGGGGGGCCTCAG
                                                                                                                                           GGAAGCC---GATGGGGTCTATGCAGCCTCAGGGGGGCCTCAG 1949
                                                                                                                                                                    ACTGCCTGGTGACAGAGAATGTCCTGAAGAATCAGTGACTTTGGGGATGTCCCGAGA
                                                                                                                                                                                                                                                                            TCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAG
                                                                                                                                                                                                                                                                                          TCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAG
                                                                                                                                                                                                                                                                                                                                AGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGCGACTTCCTGACCTTCC
                                                                                                                                                                                                                                                                                                                                                                                   CNAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is human protein kinase cDNA
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 (first entry)
                                                  CDNA;
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                                                  361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 296.2; DB 1
Pred. No. 1.9e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Human; ss; protein kinase; minel6676human sl; cancer; cytostatic; antianginal; hypotensive; cardiant; prollferative disorder; cardiovascular disorder; heart failure; cellular growth related disorder; cardiovascular disorder; heart failure; hypertension; atrial fibrillation; dilated cardiomyopathy;
                                                                                                                                                                                                                                                                                    31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                US6465232-B1
                                                                                                                                                                                                                                                                                                                                                                                                      Human protein kinase cDNA mine16676human_s1.
                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                  07-SEP-2001; 2001US-00948802.
                                                                                                                                                                                                                                                                                                                  15-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                             idiopathic cardiomyopathy; angina.
                                                                                                                                                                                                                                                                                                                                              sapiens.
                                                                                                                                                                                                                                           2003-147067/14.
                                                                                                                                                                                                                                                                                     99US-00387212
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Novel human kinase and phosphatase nucleic acid molecules useful treating cellular proliferative disorders such as cancer, cardiov diseases, hypertension, heart failure and angina. cardiovascular

Claim 7; Fig 5; 47pp; English.

The invention relates to an isolated human kinase and phosphatase nucleic CC acid molecule appearing as ABX14972, ABX14973, ABX14975, ABX14976, and CC ABX14978-ABX14981, or their complement. Also included are: (1) an CC isolated nucleic acid molecule which is at least 90 % identical to the CC nucleotide sequence ABX14973 or ABX14975, or 95 % identical to the CC nucleotide sequence ABX14973 or ABX14975, or 95 % identical to the CC complement, where the nucleic acid molecule encodes a polypeptide having CC a kinase activity; (2) An isolated nucleic acid molecule which hybridises CC to ABX14973, ABX14976, and ABX14978 in 6X saline sodium citrate (SSC) at 45 plusoC, followed by one or more washes in 0.2X SSC, 0.1% cC sodium dodecyl sulphate (SDS) at 65 plusoC, where the molecule encodes a CC polypeptide with kinase activity; (3) a vector comprising the CC compressing a polypeptide by culturing a host cell comprising the CC compressing a polypeptide by culturing a host cell comprising the CC confisation probes for detecting which the nucleic acid molecule is expressed. CC feelular processes, and fragments are useful as primers or CC hybridisation probes for detecting kinase and phosphatase encoding cardiovascular disorders such as cancer and cellular growth related disorders including cardiovascular disorders such as heart failure, hypertension, atrial CC campina. The present sequence is one of the human kinase or phosphatase cDNAs of the invention

Sequence 361 BP; 71 A; 101 C; 120 G; 68 T; 0 U; 1 Other;

13.1%;

Score 296.2; DB 10; Pred. No. 1.9e-46;

Length

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Best Local Similarity
Matches 333; Conserv
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             TCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAG 1792
                                                                                   CNAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCC
                                                                                                                           Conservative
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Search completed: March 19, 2005, 04:31:26 Job time : 1087.29 secs	320 GGAAGCCCGATTGGGGGTCTATGCAGCCTCAGGGGGCCTCAG 361	1911 GGAAGCCGATGGGGTCTATGCAGCCTCAGGGGGGCCTCAG 1949	260 ACTGCCTGGTGACAGAGAAGAATGTCCTGAAGAATCAGTGACTTTGGGGATGTCCCGAGA 319	1853 ACTGCCTGGTGACAGAGAAGAATGTCCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA 1910	200 CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA 259	1793 CTGCTGGCATGGAGTACCTGGAGCAAGTGCTGCATCCACCGGGACCTGGCTGG

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Result
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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## ALIGNMENTS

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1201 CTCCTGCAGGATGACCGCCACTCCACGTCCTCCGGAGCAGGAGCGAGAGGGGAAGG 1260	312 AGGGCCTTAGACCCCCTTGCTCCGGCGAACACCCCAACACCCCAACACCCCCCCC
RESULT 2 LACUS LOCUS DEFINITION Sequence 1 from patent US 6686187.  AR456323 VERSION AR456323 VERSION AR456323 VERSION AR456323 VERSION AR456323 ORGANISM Unclassified.	Db 1392 AACCTGTACCGACTGGAAGGGGAAGGCTTTCCTAGCATTCCTACCACCACT, 1451  Oy 1361 CTGGACACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

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8	B 8	B &	dg VQ	4d 6	g Q	Query M Best Lo Matches	NIELAO	JOURNAL FEATURES	AUTHORS	ORGANIS	ACCESSION VERSION KEYWORDS	RESULT 3 CQ725220 LOCUS	₽ \$					
301 AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG 360	241 GAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAGGGCCCCTGAGC 300	181 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCTGGGCTGAGATCACCAGCCAG	121 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC 180	GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGTCAAGAGT	TCTTCTGAGC	Query Match 90.2%; Score 2036; DB 6; Length 2697; Best Local Similarity 91.5%; Pred. No. 0; Matches 2256; Conservative 0; Mismatches 0; Indels 210; Gaps 1;	/dr /mc /dr	Patent: WO 02068579-A 11154 06-SEP-2002; PE Corporation (NY) (US) PE Corporation (NY) (US) 1 02697		-	CQ725220 CQ725220.1 GI:42286077		221 IACCHOGANGCIGCAGAGCATCCGAAAAGCGGCATCGG 2327 2292 TACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCGG 2327	TAGGERGA GEORGE CONTROL CONT	THE TRANSPORT OF THE		TOSCIAL TARCIA CONCUENTA CALLO CONTROL	1 אין
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1321 TACCACGGGGCCATCCCGAGGGCAGAGGTGGCTGAGCTGCTGGTGCACTCTGGGGACTTC 1450	31 CTCCCTCCACCGCTGCAGCTCATTCCGGAGGTGCAGAAGCCCCTGCATGAGCAGCTGTGG 13			CAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCCCCGCCTGTGCTG	1 CAAGAACCACTGCAGGGCTGCAGGTAGCGCTGTGCAGCCCAAGCTGCAGGCCCAG 	GAAGAGAAACACCCACCCCCGGGAGCGGGTGCAGCTGCTGGGCAAGAGGCAAGTGCTG	961 ACCGAGATGGTGTACAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGGAGCTCCGGAAT 1020 	901 CTGACTGTGGAGAGCGTGCAGCACACGCTGACCTCAGTGACAGATGAGCTGGCTG	841 GATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGAGCTCCAGCTGAACGAG 900	781 TACCAAGGCTTCCTGCGACAGTATGGGTCCGACCTGACGTCCCACCCTGTGTCACGTTC 840	721 GTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCCCGCATCCAGCCTGAGGCTGAG 780	661 TGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGTGCAGGATGAG 720	601 CACCAGCTCCTGCCCGGCCTGCTGCGGTCACTGCAGGACCTGCACGAGGAGGAGATGGCT 660	541 GCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCGCAGCACCACCACCACCACCAC 600	481 AAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGGCTGTGGAAGCTCTTT 540	421 CAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAG	361 CAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAGC 420	311 AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG 370

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Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Wadan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 51 Row: e Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 13376997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, &
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
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Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens feline sarcoma c
IMAGE:5170548), complete cds.
BC035357
BC035357.1 GI:23271524
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ilarity 91.5%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2771)

Alcalay,M., Antolini,F., Van de Ven,W.J., Lanfrancone,L., Grignani,F. and Pelicci,P.G.

Characterization of human and mouse c-fes cDNA clones and
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Homo sapiens (human)
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//protein id="CAA36438.1"
//b_xref="G1:29891"
//db_xref="G1:29891"
//db_xref="GOA:P07332"
//db_xref="GOA:P07332"
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//db_xref="GOA:P07332"
//db_xref="MoiProt/Swiss-Prot:P07332"
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//translation="MosSelCSpQGHGVLQMAEITSQTEGLSRLLRQHAEDLNSGFLSKL
SLLIRERQLEKTYSEGWQQLQGELTKTHSQDIEKLKSQYRALLARDSAQAKRKYQEAS
KDKDRDKAKDKYVRSLWKLFAHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHEE
MACILKEILQEYLEISSLVQDEVVAIHEMAAAARIQPEAEYGFLRQYGSAPDVPP
CVTPDESLLEEGEPLEPGELQLNELTVESVQHTLTSVUDELAVATEMVFRRQEMVTQL
QQELRNEEENTHPRERVQLLGKRQVLQEALQGLQVALCSQAKLQAQQELLQTKLEHLG
PGEPPPVLLLQDDRHSTSSSEGEREGGRTFTLSILKSHISGIFRPKFSLPPPLQLIPE
VQKPLHEQLWYHGAIPRAEVAELLVHSGDFLVRESQGKQEYVLSVLUGGLQELLQTKLEHLG
PGEPPVLLLQDDRHSTSSSEGEREGGRTFTLSILKSHISGIFRPKFSLPPPLQLIPE
VQKPLHEQLWYHGAIPRAEVAELLVHSGDFLVRESQGKQEYVLSVLUGGLQELLQTKLHGQ
LIGRGNFGEVESGRLRADNTLVAVKSCRETLPPDLKAKFLQEARILKQYSHPNIVRLIG
VCTQKQPIYIVMELVQGGDFLTFLFTEGARLRVKTLLQMVGDAAAGMEYLESKCCIHR
DLAANNCLVEKNVLKISDFGWSREEADGVYAASGGSRQVFVKWTAFBEALNGRYSSE
SDVWSFGILLMETFSLGASPYPNLSNQQTREFVEKGGRLPCPELCPDAVFRLMEQCWA
YTSPGQRPSFSTIYQELQSIRKNHR"

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mol_type="mRNA"
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Best Local Similarity
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Genes expressed in foam cell differentiation
Genes: WO 0177389-A 256 18-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shiffman, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                             TTGCATCCTGAAGAATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGTGCAGGATGA
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  GTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCTGTGTCACGTT
                            GGTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCCCGCCATCCAGCCTGAGGCTGA
                                             GGTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCCCGCATCCAGCCTGAGGCTGA
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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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91.4%;
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GCGTCTCATTGGTGTCTGCACCCAGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCA
                                                                                             GCGAGCCGACAACACCCTGGTGGCGGTGAAGTCTTGTCGAGAGACGCTCCCACCTGACCT
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                                          CAAGGCCAAGTTTCTACAGGAAGCGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGT
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                                                                                                                          GCGAGCCGACAACACCCTGGTGGCGGTGAAGTCTTGTCGAGAGACGCTCCCCACCTGACCT
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Wilks,A.F. and Kurban,R.R.
Isolation and structural analysis
Oncogene 3 (3), 289-294 (1988)
89083198
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Mouse c-fes proto-oncogene mRNA
X12616
X12616.1 GI:50955
X12616.1 GI:50955
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                               proto-oncogene;
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Sciurognathi; Muridae;
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GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGGCCAGAGC
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Pred. No. 2.5e-258;
0; Mismatches 296; I
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MEDLINE
PUBMED
   SGS
                                                             source
                                                                                                                                                           ACFTS140A

2715 bp ss-RNA linear VRL 27-APR-1993

ION Pujinami sarcoma virus temperature sensitive (ts) p140 transforming
protein RNA, 3' end.

NM14930

M14930.1 GI:209688

S transforming protein.
Pujinami sarcoma virus
Pujinami sarcoma virus
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.

CE 1 (bases 1 to 2715)

CCB 1 (bases 1 to 2715)

RS Chen,L.H., Hatada,E., Wheatley,W. and Lee,W.H.

RS Single amino acid substitution, from Glu1025 to Asp, of the fps
oncogenic protein causes temperature sensitivity in transformation
and kinase activity
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87044080
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/mol_type="genomic RNA"
/db_xref="taxon:11885"
<1. .2697
                                                           Location/Qualifiers
1. .2715
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Query Match
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nilarity 66.2%;
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/protein_id="AAA42403.1"
/db_xref="GI:209689"
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                                                                                                                                                c-myc proto-oncogene; complete genome; fps oncogene; polyprotein. Fujinami sarcoma virus Fujinami sarcoma virus Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.

1 (bases 1 to 4788)
1 (bases 1 to 4788)
Shibuya, M. and Hanafusa, H.
Nucleotide sequence of Fujinami sarcoma virus: evolutionary relationship of its transforming gene with transforming genes of other sarcoma viruses
Cell 30 (3), 787-795 (1982)
                                                                                                                                                                                                                                                                                                                 4788 bp 88-RNA linear VRL 2 Pujinami 8arcoma virus (unintegrated circular), complete J02194 K01827 K01828 J02194.1 GI:209686
                                                               2 (bases 1832 to 1881; 2851 to 2902)
Carlberg, K., Chamberlin, M.E. and Beemon, K.
The aylan sarcoma virus PRCII lacks 1020 nucleotides of the
transforming gene
Virology 135 (1), 157-167 (1984)
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The sequence of 1182 amino acids was deduced from the Fujinami sarcoma virus (FSV) transforming protein p130, the product of gag-fps fused gene. p130 is highly homologous to the gag-fes sequence of feline sarcoma virus (see separate entries), and is homologous in the 280 residue carboxyl end (including the
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                                      GACAGGGAGTATGCAGGACTGCTTCACCACATGTCC------CTGCAGGACAGT 168
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SQRAKSDREYAGMLHHMFSOLEKQEGLGHLRAYDHSSOLESWWYLASQOTETLSQYTR
RHABELAAGPLAKLSILIRDKQOLRKVFSEQWQOLSOBYAWTTQQBUSKLKAQYRSLV
RDSTQAKKKYGBASKDKEREKAKEKYYRSLSKLYALHNQYVLAYQAALLHHHHYQRA
LPTILHESLYSLQQEWYLVLKEILGEXCSITSLVQEDVLAIHGKYAHAVEMIDPATEYS
SFVQCHRYDSEVPPAVTFDESLLEEARNLEFGELQUAELTIESVQHSLTSIEEELLAS
RKAVSSKEQRWWELQYELRGEELALSPGERVHLLGKRQGIREAQQQLQGLVCAQAKLQ
AQRDMLANKLAELGSEEPPPALFLQBDRQSARSTDQERSGYTALKTIKHHISGIFSPR
FSLPPPVPLIPEVQKPLCQQAWYHGAIPRSEVQELKYSGDFLVRESQGKQEYVLSVL
WDGQPRHFIIQADNLYRLEDGLPTIPLLIBHLQSQRPITRKSGIVLTRAVLKOKW
VLNHEDVLKGERIGRGRYVSGRLHADNFPVAVKSCRETLPPELKAKFLQEARILK
QCNHPNIVRLIGVCTQKOPIYIWBLVQGGDFLSFIRSKGPRLKMKKLIKMMENAAAG
MEYLBSKHCHRDLAARNCLVTEKNTLKISDFGMSRQEBDGVYASTGGMKQIPVKWTA
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[ proviral genome; 768 bp upstream of SmaI site.
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Submitted (12-NOV-1997) NIH,
20894, USA
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RETROVIRUSES: 757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petropoulos, C.J.
Appendix 2: Retroviral taxonomy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujinami sarcoma virus
Viruses; Retroid viruses;
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//protein pl40 polyprotein"
//protein_id="p140 polyprotein"
//protein_id="hACG2565.1"
//protein_id="hACG2565.1"
//db_xref="g1:2801467".1"
//db_xref="g1:2801467
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MEYLESKHCIHRDLAARNCLVTEKNTLKISDFGMSRQEEDGVYASTGGMKQIPVKMTA
PEALNYGWYSSESDVWSFGILLWEAFSLGAVPYANLSNQQTREAIEQGVRLEPPEQCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Fujinami sarcoma virus"
/mol_type="genomic RNA"
/db_xref_"taxon:11885"
                     /product="CA"
1307. .3925
                                                                                                        /product="p14 MA"
899. .1087
                                                                                                                                                                  EDVYRLMQRCWEYDPHRRPSFGAVHQDLIAIRKRHR"
                                                                /product="p10"
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Van Groningen, J.J., Van den Ouweland, A.M., Verbeek, J.S., Vemp, A.W., Bloemers, H.P. and Van de Ven, W.J.

Structural analysis of a variant clone of Snyder-Theilen
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Figure 4. Nucleotide sequence
clone of ST-FeSV.
M22820 GI:340749
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                                         CAGACCAAGCTGGAGCACCTGGGGCCCGGGCGAGCCCCGGCCTGTGCTGCTCCTGCAGGAT
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                            /organism="unclassified"
/mol_type="unassigned DNA"
/db_xref="taxon:12908"
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mat_peptide	2083 AGCAATCAGCAGACACGGGAGTTTGTGGAGAAGGGGGGGCCGTCTGCCCTGCCCAGAGCTG 2142	ઠ
mat_peptide	3074 AGCTTCGGCATCTTGCTATGGGAGACCTTCAGCCTGGGCGCCTCCCCCTACCCCAACCTC 3133	DЬ
mat_peptide	2023 AGCTTTGGCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTC 2082	Ş
mat_peptide	1963 AAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGG 2022	B 8
	1903 TCCCGAGAGGAAGCCGATGGGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCCGTG 1962	ß 8
	1843 GCTGCTCGGAACTGCCTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATG 1902 	g &
	1783 GGGGATGCAGCTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTG 1842	B 8
	1723 CTGACCTTCCTCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTG 1782	g &
GD <sub>A</sub>	1663 GTCTGCACCCAGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGG	g 9
FEATURES source		Db
sequence for pres	CTACAGGAAGCGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGT	<b>5</b> 8
virus (s sequence authors	1543 ACCCTGGTGGCGGTGAAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTT 1602	B &
with tyr sequence (a) str	1483 GAGCAGATTGGACGGGGAACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAAC 1542	B 8
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Viruses; retrovir	2354 ATCATCCAGTCCGCTGACAACCTCTACCGACTGGAAGGAGGTGGCTTTGCGAGCATCCCC 2413	₽
MS	AACCTGTACCGACTGGAAGGGGAAGGCTTTCCTAGCATTCCT	8
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cansforming polyprotein of the snyder-theilen strain of feline a virus (fesv) include the transforming gene (fes) product yrosine specific protein kinase activity, the encoded protein train (see fesvgaone), fps gene products of gardner-arnstein ttrain (see fesvgaone), fps gene of avian fujinami sarcoma (see fsv), and src gene of avian sarcoma virus, the reported ne contains a 145bp deletion against the ga strain, and the sargue that they sequenced a defective clone, the missing bides are denoted by n's (see fesvgaone between 1818 and 1964 resumed base sequence), the last 24 bases represent the ce of feline leukemia virus.
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A., Laprevotte, I., Galibert, F., Fedele, L.A. and Sherr, C.J. tide sequences of feline retroviral oncogenes (v-fes) provide ce for a family of tyrosine-specific protein kinase genes (2) (3), 775-785 (1982)
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sarcoma virus
                           /product="protein p30"
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                                                                                             'product="protein
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/mol_type="genomic RNA"
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                                                         CTTCAGGAAGCAAAGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATCGGC
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                                                                                                                                                                                                                                 the transforming polyprotein of the gardner-arnstein strain of feline sarcoma virus (fesv) include the transforming gene (fes) product with tyrosine specific protein kinase activity. the encoded protein sequence was compared with the gene products of snyder-theilen strain (see fesvstone), fps gene of avian fujinami sarcoma virus (see fesv), and src gene of svian sarcoma virus. the last 24 bases represent the sequence of feline leukemia virus. Location/Qualifiers
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Hampe, A., Laprevotte, I., Galibert, F., Fedele, L.A. and Sherr, C.J.
Nucleotide sequences of feline retroviral oncogenes (v-fes) provide
evidence for a family of tyrosine-specific protein kinase genes
Cell 30 (3), 775-785 (1982)
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/proteIn_id="AAA43041.1"
/db_xref="GI:323873"
/db_xref="GI:323873"
/translation="MGQTITTPLSLTLDHWSEVRARAHNQGVEVRKKKWITLCEAEWV
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PGGHGPPPSGPRTPTASPIASFLRERRENPAEESQALPLREGPNNRPQYWPFSASDLY
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                      ACTCTGGTGGCCGTGAAATCTTGTCGCGAGACACTCCCACCTGACATCAAGGCCAAGTTT
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200bp upstream from a bglii site.
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YQBASKDKDRDKAKLEQLGPGEP PVLLLQDDRHSTSSSEQREEGGRPPTLE ILKSHI
SGIFREKFSLPPPLQLVPEVQKPLHEQLWYHGALPAREVAELLTHSGDELVRESQGKQ
EYVLSVLWDGQPRHFIIQSADNLYR PEGDGPASIPLLVDHLLESQQPLTKKSGIVLNR
AVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDIKAKFL
QBAKILKQYSHPNIVRLJGVCTYQKPIYIVMELVQGGDPLTFLEGARLRMKTILQM
VGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFMSREAADGIYAASGGLRQ
VVKWTAPEALMYGRYSSESDVWSFGILLWETTSLGASPYPNLSNQQTREFVEKGGRL
PCPELCPDAVFRLMEQCWAYEPGQRPSFSAIYQELQSIRKRHR"
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PGEDGRPTQLENVIDETFPLTRENWDFATPAGREHLRLYRQLLLAGLICGARRENYNLA
QVKQVVQKEETPPAARADGTWGFSEILCSPQGHGAEQQMCAFLELLEGGMCKWMVSQ
VKSDREYAGLLHHMSLQDGGGRGTGPYSPISQSWAEITSQTEĞLSRLLLRQHAEDLNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="protein 592. .1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="protein p30"
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Pred. No. 2.8e-131;
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BC073445
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                                                            CE 2 (bases 1 to 4788)

CE 2 (bases 1 to 4788)

Strausborg, R. L., Peingold, E. A., Grouse, L. H., Derge, J.G.,

Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,

Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,

Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,

Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,

Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,

Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,

McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S.,

Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,

Villalon, D. K., Muzny, D. M., Sodergren, B. J., Lu, X., Gibbs, R. A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,

Boutfard, G. G., Bakesley, R. W., Touchman, J. W., Green, B. D.,

Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M.,

Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E.,

Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 4788)
Klein,S.L., Strausberg,R.L., Wagner,L., Pontius,J., Clifton,S.W.
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Xenopus laevis MGC80946 protein, IMAGE:5516233), complete cds
                  Generation and initial analysis of more than 15,000 human and mouse cDNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Richardson, P.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis
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Matches 1421; Conserv
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: XGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Canada

Contact Agency, Vancouver, BC, Canada
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Submitted (14-JUN-2004) National Institutes of Health, Xenopus Gene Submitted (XGC), National Institute of Child Health and Human Collection (XGC), National Institute of Child Health, Xenopus Gene Collection (XGC), National Institute of Child Health, Xenopus Gene Collection (XGC), National Institutes of Health, Xenopus Gene Collection (XGC), National Institutes of Health, Xenopus Gene Collection (XGC), National Institutes of Child Health, Xenopus Gene Collection (XGC), National Institutes of Health, Xenopus Gene Collection (XGC), National Institutes of Health, Xenopus Gene Collection (XGC), National Institutes of Child Health and Human Gene Collection (XGC), National Institutes of Child Health and Human Gene Collection (XGC), National Institutes of Child Health and Human Gene Collection (XGC), National Institute of Child Health and Human Gene Collection (XGC), National Institute of Child Health and Human Gene Collection (XGC), National Institute of Child Health and Human Gene C
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20892-7510, USA
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IHQEMVQILKNIMQBYSBITSLVQBEVVSLHREIASANIRISPEQEXINFLQMKRSVS
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IGKGNFGEVFSGRLRANNTPVAVKSCRDTLPFDLKDKFLMEARILKQYSHPNIVKLIGR
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DLAARNCLVTEKNALKISDFGWSREEBDGVYSSTGGMKQIPIKTAPBALNYGRYSSE
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399. .2867
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LSKLTILIREKQQLKKSYSEQWQLLNQDYMKTTQQDIEKLRCQYRSQVKETFQSKRKY
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                                                                                                                                                                                                                                                                                                                            SDVWSFGILLWEAFSLGSVPYAAMTNQQTREAIEQGVRLLVPDNCPDEVYSLMLRCWE
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/tissue_type="Embryo, stage 31/32,
/clone_lib="NICHD_XGC_Emb4"
/lab_host="DH10B"
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/mol_type="mRNA"
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                                           Score 656.4; DB 5;
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Van de Ven,W.J.M., Roebroek,A.J.M. and Schalken,J.A.
Recombinant DNA and cDNA, mRNA, protein, antibodies, and a method of detecting tumor cells
Patent: EP 0246709-A 2 25-NOV-1987;
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100.0%; Pred. No. 1.4e-100;
ive 0; Mismatches 0;
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